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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:09:44 ; Search time 28 Seconds
(without alignments)
29.326 Million cell updates/sec

Title: US-10-827-133-9
Perfect score: 11
Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	3	US-09-056-105-33
2	11	100.0	11	3	US-09-425-585-1
3	11	100.0	11	4	US-09-953-321-1
4	11	100.0	11	4	US-08-756-416-1
5	5	45.5	25	3	US-09-443-501A-1
6	5	45.5	38	2	US-08-484-905-85
7	5	45.5	38	3	US-08-481-985B-85
8	5	45.5	38	3	US-08-370-476-85
9	5	45.5	41	4	US-09-493-795B-316
10	4	36.4	5	6	5217869-73
11	4	36.4	5	6	5227466-25
12	4	36.4	5	6	5217869-73
13	4	36.4	5	6	5227466-25
14	4	36.4	8	1	US-08-079-741A-101
15	4	36.4	8	1	US-07-939-065A-101
16	4	36.4	8	3	US-08-688-988-48
17	4	36.4	9	1	US-08-036-555B-27
18	4	36.4	9	1	US-08-469-569-27
19	4	36.4	9	1	US-08-249-322A-27
20	4	36.4	9	1	US-08-467-083-26
21	4	36.4	9	1	US-08-469-526A-27
22	4	36.4	9	1	US-08-414-417B-26
23	4	36.4	9	2	US-08-486-348A-26
24	4	36.4	9	2	US-08-734-591A-27
25	4	36.4	9	2	US-08-468-545B-26
26	4	36.4	9	2	US-08-469-660-27
27	4	36.4	9	3	US-08-396-385-12

28	4	36.4	9	3	US-08-159-339A-151	Sequence 151, App
29	4	36.4	9	3	US-08-159-339A-164	Sequence 164, App
30	4	36.4	9	3	US-08-159-339A-165	Sequence 165, App
31	4	36.4	9	3	US-08-159-339A-166	Sequence 166, App
32	4	36.4	9	3	US-08-159-339A-167	Sequence 167, App
33	4	36.4	9	3	US-08-159-339A-168	Sequence 168, App
34	4	36.4	9	3	US-08-159-339A-169	Sequence 169, App
35	4	36.4	9	3	US-08-159-339A-170	Sequence 170, App
36	4	36.4	9	3	US-08-159-339A-171	Sequence 171, App
37	4	36.4	9	3	US-08-466-680B-26	Sequence 26, Appl
38	4	36.4	9	3	US-08-470-335-27	Sequence 27, Appl
39	4	36.4	9	3	US-08-735-021-27	Sequence 27, Appl
40	4	36.4	9	3	US-08-734-664A-27	Sequence 27, Appl
41	4	36.4	9	3	US-08-470-339-27	Sequence 27, Appl
42	4	36.4	9	3	US-09-287-221-12	Sequence 12, Appl
43	4	36.4	9	4	US-08-467-602-27	Sequence 27, Appl
44	4	36.4	9	4	US-09-354-533-26	Sequence 26, Appl
45	4	36.4	9	4	US-09-056-461-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-056-105-33
; Sequence 33, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: E.Coli
US-09-056-105-33

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYALAA 11
Db 1 AANDENYALAA 11

RESULT 2

US-09-425-585-1
; Sequence 1, Application US/094255585
; Patent No. 6348315
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT

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; ORGANISM: Escherichia coli
US-09-425-585-1

Query Match
Best Local Similarity 100.0%; Score 11; DB 3; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYALAA 11
Db 1 AANDENYALAA 11

RESULT 3
US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYALAA 11
Db 1 AANDENYALAA 11

RESULT 4
US-08-756-416-1
; Sequence 1, Application US/08756416
; Patent No. 669715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Fell, Perry
; APPLICANT: Mittler, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
; TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755
; FILING DATE: 30-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.41US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-756-416-1

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYALAA 11
Db 1 AANDENYALAA 11

RESULT 5
US-09-443-501A-1
; Sequence 1, Application US/09443501A
; Patent No. 6303342
; GENERAL INFORMATION:
; APPLICANT: Kosan Biosciences, Inc.
; APPLICANT: Julien, Bryan
; APPLICANT: Katz, Leonard
; APPLICANT: Khosla, Chaitan
; APPLICANT: Tang, Li
; APPLICANT: Ziermann, Rainer
; TITLE OF INVENTION: Recombinant Methods and Materials for Producing
; TITLE OF INVENTION: Epothilone and Epothilone Derivatives
; FILE REFERENCE: 30062-20031.00
; CURRENT APPLICATION NUMBER: US/09/443,501A
; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 60/130,560
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/122,620
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: US 60/119,386
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/109,401
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-443-501A-1

Query Match
Best Local Similarity 100.0%; Score 5; DB 3; Length 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YALAA 11
Db 14 YALAA 18
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RESULT 6

US-08-484-905-85
; Sequence 85, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484.905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14..15
; OTHER INFORMATION: /note= "xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
US-08-484-905-85

Query Match 45.5%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

6 NYALA 10

Db

8 NYALA 12

RESULT 7

US-08-481-985B-85
; Sequence 85, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14..15
; OTHER INFORMATION: /note= "xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
US-08-481-985B-85

Query Match 45.5%; Score 5; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

6 NYALA 10

Db

8 NYALA 12

RESULT 8

US-08-370-476-85
; Sequence 85, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

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; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14..15
; OTHER INFORMATION: /note="Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
; US-08-370-476-85

Query Match 45.5%; Score 5; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 8 NYALA 12

RESULT 9
US-09-493-795B-316
; Sequence 316, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-179 A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 316

; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus catus
; US-09-493-795B-316

Query Match 45.5%; Score 5; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDE 5
Db 7 AANDE 11

RESULT 10
5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73:
; LENGTH: 5
; 5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAND 4
Db 2 AAND 5

RESULT 11
5227466-25
; Patent No. 5227466
; APPLICANT: DEMEYTS, PIERRE
; TITLE OF INVENTION: INSULIN RECEPTOR BINDING SITE
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/213,918
; FILING DATE: 30-JUN-1988
; SEQ ID NO:25:
; LENGTH: 5
; 5227466-25

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAL 9
Db 1 NYAL 4

RESULT 12
5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73:
; LENGTH: 5
; 5217869-73
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Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
Db 2 AAND 5

RESULT 13
5227466-25
; PATENT NO. 5227466
; APPLICANT: DENEYS, PIERRE
; TITLE OF INVENTION: INSULIN RECEPTOR BINDING SITE
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/213,918
; FILING DATE: 30-JUN-1988
; SEQ ID NO:25:
; LENGTH: 5
5227466-25

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAL 9
Db 1 NYAL 4

RESULT 14
US-08-079-741A-101
; Sequence 101, Application US/08079741A
; Patent No. 5585275
; GENERAL INFORMATION:
; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
; APPLICANT: Johnson, Charles R.
; APPLICANT: Giebel, Lutz B.
; TITLE OF INVENTION: Pilot Apparatus For Peptide
; TITLE OF INVENTION: Synthesis and Screening
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel
; ADDRESSEE: ROSENBLUM, PARISH & ISAACS
; STREET: 160 W. Santa Clara Street, Suite 1500
; CITY: San Jose
; STATE: California
; COUNTRY: USA
; ZIP: 95113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
; MEDIUM TYPE: storage
; COMPUTER: IBM Clone
; OPERATING SYSTEM: MS-DOS 5.00
; SOFTWARE: WordPerfect 5.1, ASCII format (DOS text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/079,741A
; FILING DATE: 18-June-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,065
; FILING DATE: 02-Sept-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DULIN, JACQUES M.
; REGISTRATION NUMBER: 24,067
; REFERENCE/DOCKET NUMBER: 5303-8
; TELEPHONE: (408) 977-0120
; TELEFAX: (408) 977-0129
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: Amino Acids

STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; FEATURE:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Biossearch Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: From 1 to 8
US-08-079-741A-101

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
Db 5 ALAA 8

RESULT 15
US-07-939-065A-101
; Sequence 101, Application US/07939065A
; Patent No. 5591646
; GENERAL INFORMATION:
; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
; APPLICANT: Johnson, Charles R.
; APPLICANT: Giebel, Lutz B.
; TITLE OF INVENTION: Method and Apparatus For Peptide
; TITLE OF INVENTION: Synthesis and Screening
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel
; ADDRESSEE: PILLSBURY MADISON & SUTRO
; STREET: Ten Almaden Boulevard, Suite 800
; CITY: San Jose
; STATE: California
; COUNTRY: USA
; ZIP: 95113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
; MEDIUM TYPE: storage
; COMPUTER: IBM Clone
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.2, ASCII format (DOS text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/939,065A
; FILING DATE: 02-Sept-1992
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NA
; FILING DATE: NA
; ATTORNEY/AGENT INFORMATION:
; NAME: DULIN, JACQUES M.
; REGISTRATION NUMBER: 24,067
; REFERENCE/DOCKET NUMBER: 5303-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 947-4000
; TELEFAX: (408) 287-8341
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 8
; TYPE: Amino Acids
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; FEATURE:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Bioscience Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; OTHER INFORMATION: determined. Xaa represents a random amino acid
; OTHER INFORMATION: selected from mixtures of the following 10 amino
; OTHER INFORMATION: acids to give equal incorporation: Nle, His, Pro,
; OTHER INFORMATION: Gln, Tyr, Gly, Phe, Arg, Glu, Ala. Where Leu or
; OTHER INFORMATION: Ala is specified at any position in the sequence,
; OTHER INFORMATION: then Leu refers to Nle (or normal-leucine) and Ala
; OTHER INFORMATION: refers to Ala (or beta-alanine).
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: 1 to 8
; US-07-939-065A-101
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Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 8 ALAA 11
Db 5 ALAA 8
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Search completed: May 5, 2005, 18:24:18
Job time : 29 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:18:20 ; Search time 78 Seconds
(without alignments)
47.046 Million cell updates/sec

Title: US-10-827-133-9
Perfect score: 11
Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1428581 seqs, 333598853 residues

Word size : 0
Total number of hits satisfying chosen parameters: 425092

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	11	100.0	11	9 US-09-953-321-1	Sequence 1, Appli
2	11	100.0	11	9 US-09-975-132A-3	Sequence 3, Appli
3	11	100.0	11	14 US-10-289-135A-119	Sequence 119, Appl
4	11	100.0	12	14 US-10-080-866-19	Sequence 19, Appl
5	6	54.5	6	14 US-10-037-243-3	Sequence 3, Appli
6	5	45.5	9	15 US-10-149-138-2806	Sequence 2806, Ap
7	5	45.5	9	15 US-10-149-138-4120	Sequence 4120, Ap
8	5	45.5	9	15 US-10-149-138-4153	Sequence 4153, Ap
9	5	45.5	9	16 US-10-149-138-2806	Sequence 2806, Ap
10	5	45.5	9	16 US-10-149-138-4120	Sequence 4120, Ap
11	5	45.5	9	16 US-10-149-138-4153	Sequence 4153, Ap
12	5	45.5	10	15 US-10-149-138-629	Sequence 629, App
13	5	45.5	10	15 US-10-149-138-2978	Sequence 2978, Ap

14	5	45.5	10	15	US-10-149-138-4331	Sequence 4331, Ap
15	5	45.5	10	15	US-10-149-138-4411	Sequence 4411, Ap
16	5	45.5	10	15	US-10-149-138-4430	Sequence 4430, Ap
17	5	45.5	10	16	US-10-149-138-629	Sequence 629, App
18	5	45.5	10	16	US-10-149-138-2978	Sequence 2978, Ap
19	5	45.5	10	16	US-10-149-138-4331	Sequence 4331, Ap
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21	5	45.5	10	16	US-10-149-138-4430	Sequence 4430, Ap
22	5	45.5	11	15	US-10-149-138-630	Sequence 630, App
23	5	45.5	11	15	US-10-149-138-757	Sequence 757, App
24	5	45.5	11	15	US-10-149-138-1221	Sequence 1221, Ap
25	5	45.5	11	15	US-10-149-138-2253	Sequence 2253, Ap
26	5	45.5	11	15	US-10-149-138-3683	Sequence 3683, Ap
27	5	45.5	11	16	US-10-149-138-630	Sequence 630, App
28	5	45.5	11	16	US-10-149-138-757	Sequence 757, App
29	5	45.5	11	16	US-10-149-138-1221	Sequence 1221, Ap
30	5	45.5	11	16	US-10-149-138-2253	Sequence 2253, Ap
31	5	45.5	11	16	US-10-149-138-3683	Sequence 3683, Ap
32	5	45.5	15	15	US-10-149-138-3747	Sequence 3747, Ap
33	5	45.5	15	15	US-10-149-138-3886	Sequence 3886, Ap
34	5	45.5	15	15	US-10-149-138-3919	Sequence 3919, Ap
35	5	45.5	15	15	US-10-149-138-4456	Sequence 4456, Ap
36	5	45.5	15	15	US-10-149-138-4511	Sequence 4511, Ap
37	5	45.5	15	16	US-10-149-138-3747	Sequence 3747, Ap
38	5	45.5	15	16	US-10-149-138-3886	Sequence 3886, Ap
39	5	45.5	15	16	US-10-149-138-3919	Sequence 3919, Ap
40	5	45.5	15	16	US-10-149-138-4456	Sequence 4456, Ap
41	5	45.5	15	16	US-10-149-138-4511	Sequence 4511, Ap
42	5	45.5	25	9	US-09-727-889-1	Sequence 1, Appli
43	5	45.5	41	17	US-10-895-372-316	Sequence 316, App
44	5	45.5	44	9	US-09-815-242-12843	Sequence 12843, A
45	4	36.4	7	9	US-09-884-767A-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYALAA 11
| | | | |
Db 1 AANDENYALAA 11

RESULT 2
US-09-975-132A-3
; Sequence 3, Application US/09975132A
; Publication No. US20020182672A1

GENERAL INFORMATION:
; APPLICANT: Kolkman, Marc
; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a
; FILE REFERENCE: GC636-2
; CURRENT APPLICATION NUMBER: US/09/975,132A
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/239,531
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide tag
US-09-975-132A-3

Query Match 100.0%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
| | | | | | | | | | |
DB 1 AANDENYALAA 11

RESULT 3
US-10-289-135A-119
; Sequence 119, Application US/10289135A
; Publication No. US20030180937A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIU, GEORGE
; APPLICANT: DELISA, MATTHEW
; TITLE OF INVENTION: ENGINEERING OF LEADER PEPTIDES FOR THE SECRETION OF
; FILE REFERENCE: CLFR-019US
; CURRENT APPLICATION NUMBER: US/10/289,135A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/337,452
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-289-135A-119

Query Match 100.0%; Score 11; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
| | | | | | | | | | |
DB 1 AANDENYALAA 11

RESULT 4
US-10-080-866-19
; Sequence 19, Application US/10080866
; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Paegle, E. Sasha
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1732R1
; CURRENT APPLICATION NUMBER: US/10/080,866

; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/274,384
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide for generating antibodies
US-10-080-866-19

Query Match 100.0%; Score 11; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
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DB 2 AANDENYALAA 12

RESULT 5
US-10-037-243-3
; Sequence 3, Application US/10037243
; Publication No. US20030134352A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, LLC.
; APPLICANT: Freimuth, Paul I
; APPLICANT: Zhang, Yian-Biao
; APPLICANT: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
; FILE REFERENCE: BSA 01-22
; CURRENT APPLICATION NUMBER: US/10/037,243
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
US-10-037-243-3

Query Match 54.5%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDEN 6
| | | | | |
DB 1 AANDEN 6

RESULT 6
US-10-149-138-2806
; Sequence 2806, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; CURRENT APPLICATION NUMBER: US 09/458,299

; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2806

Query Match 45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
| | | | |
Db 5 NYALA 9

RESULT 7

US-10-149-138-4120
; Sequence 4120, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4120

Query Match 45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
| | | | |
Db 4 NYALA 8

RESULT 8

US-10-149-138-4153
; Sequence 4153, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4153
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4153

Query Match 45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
| | | | |
Db 5 NYALA 9

RESULT 9

US-10-149-138-2806
; Sequence 2806, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2806

Query Match 45.5%; Score 5; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
| | | | |
Db 5 NYALA 9

RESULT 10

US-10-149-138-4120
; Sequence 4120, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4120

Query Match 45.5%; Score 5; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 4 NYALA 8

RESULT 11
US-10-149-138-4153
; Sequence 4153, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4153
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4153

Query Match 45.5%; Score 5; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 5 NYALA 9

RESULT 12
US-10-149-138-629
; Sequence 629, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-629

Query Match 45.5%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 6 NYALA 10

RESULT 13
US-10-149-138-2978
; Sequence 2978, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2978
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2978

Query Match 45.5%; Score 5; DB 15; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; DB 15; Length 10;
QY 6 NYALA 10
Db 6 NYALA 10

RESULT 14
US-10-149-138-4331
; Sequence 4331, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4331
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4331

Query Match 45.5%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; DB 15; Length 10;
QY 6 NYALA 10
Db 6 NYALA 10

RESULT 15
US-10-149-138-4411
; Sequence 4411, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4411
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4411

Query Match 45.5%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 NYALA 10
Db 6 NYALA 10

Search completed: May 5, 2005, 18:31:04
Job time : 79 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:01:24 ; Search time 92.3333 Seconds
(without alignments)
61.006 Million cell updates/sec

Title: US-10-827-133-9
Perfect score: 11
Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	26	Q9UC79	Q9uc79 homo sapien
2	10	90.9	10	P96306	P96306 aeromonas s
3	10	90.9	10	P96321	P96321 escherichia
4	10	90.9	10	P96352	P96352 marinobacte
5	10	90.9	10	Q93LE5	Q93LE5 photobacter
6	6	54.5	9	Q93LE4	Q93LE4 heliobacill
7	6	54.5	10	P96423	P96423 pseudomonas
8	5	45.5	10	P96421	P96421 neisseria g
9	5	45.5	14	P96350	P96350 legionella
10	5	45.5	35	Q9GKJ8	Q9GKJ8 sus scrofa
11	5	45.5	49	Q9GKU9	Q9GKU9 yersinia pe
12	5	45.5	50	1 H0KE_SCOLI	P77091 escherichia
13	4	36.4	8	Q62528	Q62528 mus spretus
14	4	36.4	12	Q7YK3	Q7YK3 ribes nevad
15	4	36.4	13	Q7M355	Q7M355 ovis aries
16	4	36.4	14	1 MAST_VESLE	P01514 veapulla lew
17	4	36.4	15	Q9TWT5	Q9TWT5 lumbricus t
18	4	36.4	15	Q9TQ55	Q9TQ55 bos taurus
19	4	36.4	15	Q93LE6	Q93LE6 chloroflexu
20	4	36.4	17	Q9K407	Q9K407 rattus norv
21	4	36.4	18	Q06514	Q06514 escherichia
22	4	36.4	19	Q99MN2	Q99MN2 rattus norv
23	4	36.4	19	Q9PST5	Q9PST5 xenopus lae
24	4	36.4	20	Q15989	Q15989 homo sapien
25	4	36.4	20	Q9R4D9	Q9R4D9 escherichia
26	4	36.4	21	Q9TRA9	Q9TRA9 bos taurus
27	4	36.4	21	Q8VILL1	Q8VILL1 mus musculu
28	4	36.4	22	Q85513	Q85513 chlamydia t
29	4	36.4	22	Q85515	Q85515 chlamydia t
30	4	36.4	24	Q8SH95	Q8SH95 brookesia p
31	4	36.4	24	Q8SH98	Q8SH98 brookesia p

32	4	36.4	24	2	Q8SHA4	Q8sha4 brookesia b
33	4	36.4	24	2	Q8SK10	Q8sk10 furcifer ca
34	4	36.4	25	2	Q708G1	Q708g1 ovis aries
35	4	36.4	25	2	Q93LX3	Q93lx3 vibrio chol
36	4	36.4	26	1	DHAB_AMEYE	P80472 amycolatops
37	4	36.4	26	2	Q9BM22	Q9bm22 euperipatoi
38	4	36.4	26	2	Q9BM24	Q9bm24 euperipatoi
39	4	36.4	26	2	Q6AD80	Q6ad80 leifsonia x
40	4	36.4	27	2	Q7RQ41	Q7rq41 plasmodium
41	4	36.4	27	2	Q9GU44	Q9gu44 scypha raph
42	4	36.4	27	2	Q8GU45	Q8gu45 scypha raph
43	4	36.4	27	2	Q31210	Q31210 mus musculu
44	4	36.4	27	2	Q700R9	Q700r9 sorghum bic
45	4	36.4	27	2	Q66269	Q66269 cucumber mo

ALIGNMENTS

RESULT 1
Q9UC79 PRELIMINARY; PRT; 26 AA.
AC Q9UC79; DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Interleukin-2 high-molecular-weight form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95217316; PubMed=7702741;
RA Ahmad Z., Ciolek D., Pan Y.C., Michel H., Khan F.R.;
RT "Purification and characterization of a high-molecular-weight form of
RT recombinant human interleukin-2.";
RL J. Protein Chem. 13:591-598(1994).
DR HSSP; P60568; 1IRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
SQ SEQUENCE 26 AA; 2887 MW; 5B768892229356ED CRC64;
Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
DB 16 AANDENYALAA 26
RESULT 2
P96306 PRELIMINARY; PRT; 10 AA.
AC P96306; DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33659;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";

```

RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 90.9%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYALAA 11
Db 1 ANDENYALAA 10

RESULT 3
P96321 ID P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Komine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
DR EMBL; U68074; AAB48024.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 90.9%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYALAA 11
Db 1 ANDENYALAA 10

RESULT 4
P96352 ID P96352 PRELIMINARY; PRT; 10 AA.
AC P96352;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OX NCBI_TaxID=2743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49840;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).

DR RNA 2:1306-1310(1996).
DR EMBL; U68077; AAB48027.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 90.9%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYALAA 11
Db 1 ANDENYALAA 10

RESULT 5
Q93LE5 ID Q93LE5 PRELIMINARY; PRT; 10 AA.
AC Q93LE5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tmRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040837; AAK83525.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 90.9%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYALAA 11
Db 1 ANDENYALAA 10

RESULT 6
Q93LE4 ID Q93LE4 PRELIMINARY; PRT; 9 AA.
AC Q93LE4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Helicobacter mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tmRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040838; AAK83526.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;

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Query Match 54.5%; Score 6; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYALAA 11
 |||||
 DB 4 NYALAA 9

RESULT 7
 P96423
 ID P96423 PRELIMINARY; PRT; 10 AA.
 AC P96423 QYDCH6;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Coded portion of proteolysis tag (Translated portion of tmRNA gene
 DE ssaA) (Fragment).
 GN OrderedLocustNames=PA0826.1;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25330;
 RX MEDLINE=97128184; PubMed=8972778;
 RA Williams K.P., Bartel D.P.;
 RT "Phylogenetic analysis of tmRNA secondary structure.";
 RL RNA 2:1306-1310(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/350233079;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Golltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; U68078; AAB48029.1; -.
 DR EMBL; AE004517; AAO42616.1; -.
 KW Complete proteome.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB544AAA CRC64;

Query Match 54.5%; Score 6; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYALAA 11
 |||||
 DB 5 NYALAA 10

RESULT 8
 P96421
 ID P96421 PRELIMINARY; PRT; 10 AA.
 AC P96421
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Coded portion of proteolysis tag (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19424;
 RX MEDLINE=97128184; PubMed=8972778;
 RA Williams K.P., Bartel D.P.;
 RT "Phylogenetic analysis of tmRNA secondary structure.";
 RL RNA 2:1306-1310(1996).
 DR EMBL; U68080; AAB48028.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41ABIA CRC64;

Query Match 45.5%; Score 5; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALAA 11
 |||||
 DB 6 YALAA 10

RESULT 9
 P96350
 ID P96350 PRELIMINARY; PRT; 14 AA.
 AC P96350;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Coded portion of proteolysis tag (Fragment).
 OS Legionella pneumophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33152;
 RX MEDLINE=97128184; PubMed=8972778;
 RA Williams K.P., Bartel D.P.;
 RT "Phylogenetic analysis of tmRNA secondary structure.";
 RL RNA 2:1306-1310(1996).
 DR EMBL; U68079; AAB48026.1; -.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1349 MW; CE5F7318D3BE7D7D CRC64;

Query Match 45.5%; Score 5; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDEN 6
 |||||
 DB 1 ANDEN 5

RESULT 10
 Q9GKJ8
 ID Q9GKJ8 PRELIMINARY; PRT; 35 AA.
 AC Q9GKJ8;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Apolipoprotein D (Fragment).
 GN Name=APOD; (Pig).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21419000; PubMed=11528129;
 RA Van Poucke M., Verle M., Tuggle C., Pitumi F., Genet C.,
 RA Van Zeveren A., Peelman L.J.;
 RT "Integration of porcine chromosome 13 maps.";
 RL Cyogenet. Cell Genet. 93:297-303(2001).
 DR EMBL; AF222912; AAG41125.1; -.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.

```
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
KW Lipoprotein.
FT NON_TER 1 1
FT TER 35 35
SQ SEQUENCE 35 AA; 4176 MW; EAA72C366D1C4AF1 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YALAA 9
DB 4 ENVAL 8

RESULT 11
ID Q8CKU9 PRELIMINARY; PRT; 49 AA.
AC Q8CKU9
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical
GN OrderedLocusNames=y2833;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler D.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR ENBL; AE013886; AAM86384.1; -
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5616 MW; 8D8372952C8B7079 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALAA 11
DB 36 YALAA 40

RESULT 12
HOKE ECOLI STANDARD; PRT; 50 AA.
ID HOKE ECOLI
AC P77091; Q9R777;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE HOKE protein.
GN Name=hoke; OrderedLocusNames=b0581.1; ORFNames=b4415;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kaiman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RX Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemura S., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=99291074; PubMed=10361310;
RA Pedersen K., Gerdes K.;
RT "Multiple hok genes on the chromosome of Escherichia coli.";
RL Mol. Microbiol. 32:1090-1102(1999).
CC -1- SIMILARITY: Belongs to the hok/gef family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR ENBL; U00096; AAT48125.1; -
DR ENBL; U82598; AAB40780.1; ALT_INIT.
DR ENBL; D90700; BAA35222.1; ALT_INIT.
DR EcoBASE; EB4049; hokE.
DR EcoGene; EGI4302; hokE.
DR InterPro; IPR000021; Hok/gef toxin.
DR Pfam; PF01848; HOK_GEF; 1.
DR PRINTS; PR00281; HOKGEFTOXIC.
DR ProDom; PD005979; Hok/gef toxin; 1.
DR PROSITE; PS00556; HOK_GEF; 1.
KW Complete proteome; Transmembrane.
FT TRANSMEM 5 25 Potential.
SQ SEQUENCE 50 AA; 5564 MW; 8AD9A981A6D46835 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALAA 11
DB 5 YALAA 9

RESULT 13
Q62528 PRELIMINARY; PRT; 8 AA.
ID Q62528
AC Q62528; (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-1998 (TrEMBLrel. 24, Last annotation update)
DE Apolipoprotein A-II (Fragment).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10096;
 RP [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN=SPRET/E1;
 RX MEDLINE=94319082; PubMed=8043949;
 RA Ko M.S., Wang X., Horton J.H., Takahashi N., Maizaki Y.,
 RA Nadeau J.H.;
 RA "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
 RL Mamm. Genome 5:349-355 (1994).
 DR EMBL; U05692; AAB60463.1; --
 DR PIR; I48935; I48935.
 KW Lipoprotein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 827 MW; 223DDDD72DC7633B CRC64;

 Query Match 36.4%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 ALAA 11
 Db ||||
 4 ALAA 7

 RESULT 14
 Q7YKC3
 ID Q7YKC3 PRELIMINARY; PRT; 12 AA.
 AC Q7YKC3;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Photosystem Q(B) protein (Fragment).
 GN Name=psbA;
 OS Ribes nevadense.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Grossulariaceae; Ribes.
 RN NCBI_TaxID=175221;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Schulteis L.M., Donoghue M.J.;
 RT "Molecular phylogeny and biogeography of Ribes (Grossulariaceae), with
 RT an emphasis on gooseberries (subg. Grossularia).";
 RL Syst. Bot. 29:77-96(2004).
 DR EMBL; AY138090; AAP92245.1; --
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1100 MW; D6210A99A26DDB02 CRC64;

 Query Match 36.4%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 ALAA 11
 Db ||||
 1 ALAA 4

 RESULT 15
 Q7M355
 ID Q7M355 PRELIMINARY; PRT; 13 AA.
 AC Q7M355;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Glutathione peroxidase (EC 1.11.1.9) (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.

OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92231574; PubMed=1567207;
 RA Gettins P., Dyal D., Crews B.;
 RT "Selenium-dependent glutathione peroxidases from ovine and bovine
 RT erythrocytes occur as longer chain forms than previously recognized.";
 RL Arch. Biochem. Biophys. 294:511-518(1992).
 DR PIR; A38929; A38929.
 DR GO; GO:0004602; F:glutathione peroxidase activity; IEA.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1169 MW; D9FDE1422E02DDDD CRC64;

 Query Match 36.4%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 ALAA 11
 Db ||||
 4 ALAA 7

 Search completed: May 5, 2005, 18:22:50
 Job time : 94.3333 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:00:34 ; Search time 101.333 Seconds
(without alignments)
41.984 Million cell updates/sec

Title: US-10-827-133-9
Perfect score: 11
Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	2	ABB84403
2	11	100.0	11	6	AAO16101 C-termina
3	11	100.0	11	7	ADE48279 TAT depen
4	11	100.0	11	7	ADF50155 S. enteri
5	11	100.0	12	5	AAE28994 Peptide u
6	6	54.5	6	7	ADL33753 Bacteriop
7	6	54.5	32	4	AAE61562 Peptide W
8	6	54.5	32	4	AAE61569 Peptide W
9	6	54.5	32	4	AAE61568 Peptide W
10	6	54.5	32	4	AAE61559 Peptide W
11	6	54.5	37	4	AAE61571 Peptide W
12	5	45.5	9	4	AAE88621 HER2/NEU
13	5	45.5	9	4	AAE88687 HER2/NEU
14	5	45.5	9	5	AAE31119 Human erb
15	5	45.5	9	8	ADN64564 HLA bindi
16	5	45.5	9	8	ADP80193 Human HLA
17	5	45.5	10	2	AAW70073 HER-2/neu
18	5	45.5	10	2	AAW47715 Immunogen
19	5	45.5	10	4	AAE88761 HER2/neu
20	5	45.5	10	5	AAU95886 Immunogen
21	5	45.5	10	5	AAU95886 Immunogen
22	5	45.5	10	8	ADN64603 HLA bindi
23	5	45.5	10	8	ADP80218 Human HLA
24	5	45.5	14	3	AAE98935 HLA class
25	5	45.5	15	2	AAE48500 Histogran
26	5	45.5	15	2	AAE48506 Histogran

26	5	45.5	15	3	AAE98844	HLA class
27	5	45.5	15	4	AAE88622	HER2/NEU
28	5	45.5	15	4	AAE88688	HER2/NEU
29	5	45.5	15	4	AAE89014	HER2/neu
30	5	45.5	15	4	AAE89069	HER2/neu
31	5	45.5	15	4	AAE88344	HER2/NEU
32	5	45.5	22	6	ABR59552	S. aureus
33	5	45.5	22	7	ADC33576	Fusion pe
34	5	45.5	23	6	ABR59554	S. aureus
35	5	45.5	25	4	AAE66876	Human Erb
36	5	45.5	25	4	AAE66877	Human Erb
37	5	45.5	38	3	AAE68253	Murine cl
38	5	45.5	38	3	AAE52907	Murine cl
39	5	45.5	38	4	AAE58668	Murine cl
40	5	45.5	41	3	AAE21594	Cone snai
41	5	45.5	41	7	ADB76849	A. gossyp
42	5	45.5	44	4	AAU37250	Staphyloc
43	4	36.4	4	2	AAE55338	Inhibitor
44	4	36.4	4	8	ADP04335	Thyropero
45	4	36.4	5	2	AAE12715	Pentapept

ALIGNMENTS

RESULT 1
ABB84403
ID ABB84403 standard; peptide; 11 AA.
AC ABB84403;
XX
XX
DT 21-OCT-2002 (first entry)
XX
DE E. coli derived aberrant protein C-terminal peptide motif.
XX
KW Tumour antigen; murine; vaccine; cellular immune response; immunogen;
KW cancer; tumour.
XX
OS Escherichia coli.
XX
PN US6287569-B1.
XX
PD 11-SEP-2001.
XX
PF 06-APR-1998; 98US-00056105.
XX
PR 10-APR-1997; 97US-0043467P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
PI Kipps TJ, Wu Y;
XX
DR WPI; 1998-583198/49.
XX
PT Generating cellular immune response in patient to target protein -
PT comprises introducing vector with nucleotide sequence encoding immunogen
PT comprising protein processing signal into cell of patient.
XX
FS Example 5; Col 6; 61pp; English.
XX
XX This invention describes a novel method for generating a cellular immune
XX response in a patient to a target protein or its fragment. The method
XX involves introducing a vector containing a nucleotide sequence encoding a
XX chimeric immunogen comprising a protein processing signal and the target
XX protein or its fragment. The immunogen is produced by the cells and
XX processed so that the target protein or its fragment is presented to the
XX patients immune system and a cellular immune response is initiated. The
XX method and vectors can be used as a form of vaccination and could be used
XX to generate a cellular immune response in patients to, e.g. cancerous
XX tumours. The cellular immune response is the predominant immune response
XX in the patient. This sequence represents an E. coli aberrant protein
XX motif described in the method of the invention. Note: The information in
XX this spec has been previously disclosed in WO199845444 however this spec

```

CC contained no sequence information
XX
SQ Sequence 11 AA;

Query Match      100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
   |||||
Db 1 AANDENYALAA 11

RESULT 2
AAO16101
ID AAO16101 standard; peptide; 11 AA.
XX
AC AAO16101;
XX
DT 27-FEB-2003 (first entry)
XX
DE C-terminal tag peptide.
XX
KW Gene therapy; vaccine; humoral immune response; cellular immune response;
KW immune response modulation; pathogenic infection; rheumatoid arthritis.
XX
OS Unidentified.
XX
PN WO200283181-A1.
XX
PD 24-OCT-2002.
XX
PF 18-APR-2002; 2002WO-AU000486.
XX
PR 18-APR-2001; 2001AU-00004468.
XX
PA (UQU ) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
WPI; 2003-075509/07.
XX
New compositions having antigens, polynucleotides encoding the antigens,
PT or antigen-presenting cells, useful for modulating an immune response,
PT e.g. for treating or preventing pathogenic infections or rheumatoid
PT arthritis.
XX
PS Disclosure; Page 35; 139pp; English.
XX
CC The invention comprises compositions for eliciting a humoral or cellular
CC immune response against a target antigen. The compositions of the
CC invention are useful for eliciting a humoral and cellular immune response
CC against a target antigen, modulating an immune response in a patient, and
CC the treatment or prophylaxis of a disease or condition. This includes
CC pathogenic infections (e.g. viral, bacterial, fungal or protozoan), or an
CC immune response to an autoantigen (e.g. rheumatoid arthritis). The
CC present amino acid sequence represents a peptide which was used in the
CC invention
XX
SQ Sequence 11 AA;

Query Match      100.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
   |||||
Db 1 AANDENYALAA 11

RESULT 3
ADE48279
ID ADE48279 standard; peptide; 11 AA.

```

```

XX ADE48279;
XX
DT 29-JAN-2004 (first entry)
XX
DE TAT dependant secretion clone #1.
XX
KW leader peptide; Twin Arginine Translocation pathway;
KW putative TAT leader peptide sequence.
XX
OS Synthetic.
XX
PN WO2003040335-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035618.
XX
PR 05-NOV-2001; 2001US-0337452P.
XX
PR 21-AUG-2002; 2002US-0337452P.
XX
PA (RERE-) RES DEV FOUND.
XX
KW Georgiou G, Delisa M;
XX
WPI; 2003-449453/42.
XX
Identifying a leader peptide that directs increased protein export in
PT bacteria by screening libraries of leader peptides for sequences that
PT allow rapid export and can rescue short-lived reporter protein from
PT degradation in cytoplasm.
XX
XX Example 7; SEQ ID NO 119; 63pp; English.
XX
CC The present sequence relates to identifying a leader peptide that directs
CC increased protein export in bacteria, optionally through the twin
CC Arginine Translocation pathway, comprises screening of libraries of
CC putative leader peptides or their mutants for sequences that allow rapid
CC export and, thus, can rescue a short-lived reporter protein from
CC degradation in the cytoplasm. The method is useful in engineering of
CC leader peptides for the secretion of recombinant proteins in bacteria.
CC The leader peptides can be used to direct or enhance protein secretion.
CC The present sequence represents a putative TAT leader peptide sequence of
CC the invention.
XX
SQ Sequence 11 AA;

Query Match      100.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYALAA 11
   |||||
Db 1 AANDENYALAA 11

RESULT 4
ADF50155
ID ADF50155 standard; peptide; 11 AA.
XX
AC ADF50155;
XX
DT 12-FEB-2004 (first entry)
XX
DE S. enteritidis protease C-terminal fragment.
XX
KW promoter; mutant; vaccine; Shine Dalgarno; probiotic bacteria;
KW regulatory gene; targeted optimisation.
XX
OS Salmonella enteritidis.
XX
PN WO2003070941-A2.
XX

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```

XX WPI; 2002-723363/78.
XX
XX New vector comprising anti-termination nucleic acid or RNA encoding the
XX polypeptide with a non-lambda promoter, useful for producing human
XX thrombopoietin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide.
XX
XX Example 2; Page 32; 70pp; English.
XX
XX The invention relates to vectors for producing a polypeptide heterologous
XX to prokaryotic cells and method for producing the polypeptide. The method
XX is useful for producing a polypeptide heterologous to prokaryotic cells.
XX The present sequence is a peptide used in the exemplification of the
XX invention
XX
XX Sequence 12 AA;
XX
XX Query Match 100.0%; Score 11; DB 5; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.00019;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 AANDENYALAA 11
XX |||||
XX DB 2 AANDENYALAA 12
XX
XX RESULT 6
XX ADL33753
XX ID ADL33753 standard; protein; 6 AA.
XX
XX AC ADL33753;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Bacteriophage T7 ssrA peptide.
XX
XX KW protein solubility; coxsackievirus and adenovirus receptor; CAR;
XX KW Bacteriophage T7; ssrA peptide.
XX
XX OS Enterobacteria phage T7.
XX
XX PN US2003134352-A1.
XX
XX PD 17-JUL-2003.
XX
XX PF 04-JAN-2002; 2002US-00037243.
XX
XX PR 04-JAN-2002; 2002US-00037243.
XX
XX (FRIE// FREIMUTH P I.
XX (ZHAN// ZHANG Y.
XX (HOWI// HOWITT J A.
XX
XX Freimuth PI, Zhang Y, Howitt JA;
XX
XX WPI; 2003-897262/82.
XX
XX Enhancing the solubility of, and promoting the adoption of native
XX conformation in a recombinantly expressed polypeptide comprises
XX expressing the polypeptide as a fusion protein with a charged N- or C-
XX terminal extension.
XX
XX Disclosure; Page 9; 21pp; English.
XX
XX The invention relates to a method of enhancing the solubility of, and
XX promoting the adoption of native protein conformation of a recombinantly
XX expressed polypeptide by expressing the polypeptide as a fusion protein
XX including a peptide extension with: net negative charge (not peptide T7A)
XX positioned at the carboxy terminus; or net charge +2 to -20, positioned
XX at the amino terminus. The nucleic acids encoding the polypeptide of
XX interest and the extension are fused and inserted into an expression
XX vector which is then introduced into a host cell in which the polypeptide
XX is produced. The polypeptide is especially one that is substantially

```

CC insoluble or inactive when expressed recombinantly without the peptide
 CC extension. The present sequence represents Bacteriophage T7 ssrA peptide,
 CC used in a fusion to demonstrate the method of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 54.5%; Score 6; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDEN 6
 |||||
 DB 1 AANDEN 6

RESULT 7
 AAB61562
 ID AAB61562 standard; peptide; 32 AA.
 XX
 AC AAB61562;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Peptide WINZIPB4 used to identify hetero-associating peptides.
 XX
 KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX
 OS Unidentified.
 XX
 PN WO200100814-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 26-JUN-2000; 2000WO-EP005922.
 XX
 PR 25-JUN-1999; 99US-00344096.
 XX
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX
 DR WPI; 2001-137954/14.
 XX
 CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX
 SQ Sequence 32 AA;

Query Match 54.5%; Score 6; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENVAL 9
 |||||
 DB 13 DENVAL 18

RESULT 8
 AAB61569
 ID AAB61569 standard; peptide; 32 AA.
 XX
 AC AAB61569;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Peptide WINZIPB10 used to identify hetero-associating peptides.
 XX
 KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX
 OS Unidentified.
 XX
 PN WO200100814-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 26-JUN-2000; 2000WO-EP005922.
 XX
 PR 25-JUN-1999; 99US-00344096.

XX
 AC AAB61569;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Peptide WINZIPB11 used to identify hetero-associating peptides.
 XX
 KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX
 OS Unidentified.
 XX
 PN WO200100814-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 26-JUN-2000; 2000WO-EP005922.
 XX
 PR 25-JUN-1999; 99US-00344096.
 XX
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX
 DR WPI; 2001-137954/14.
 XX
 CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX
 SQ Sequence 32 AA;

Query Match 54.5%; Score 6; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENVAL 9
 |||||
 DB 13 DENVAL 18

RESULT 9
 AAB61568
 ID AAB61568 standard; peptide; 32 AA.
 XX
 AC AAB61568;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Peptide WINZIPB10 used to identify hetero-associating peptides.
 XX
 KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX
 OS Unidentified.
 XX
 PN WO200100814-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 26-JUN-2000; 2000WO-EP005922.
 XX
 PR 25-JUN-1999; 99US-00344096.

XX (UYZU-) UNIV ZUERICH.
 XX Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX WPI; 2001-137954/14.
 DR Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX Claim 6; Page 41; 56pp; English.
 XX The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX Sequence 32 AA;
 SQ
 Query Match 54.5%; Score 6; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DENVAL 9
 Db 13 DENVAL 18
 RESULT 10
 AAB61559
 ID AAB61559 standard; peptide; 32 AA.
 XX AC AAB61559;
 XX 03-APR-2001 (first entry)
 DT Peptide WINZIPB1 used to identify hetero-associating peptides.
 DE Hetero-associating coiled-coil peptide; heterodimerisation.
 XX KW Unidentified.
 XX OS WO200100814-A2.
 XX PN 04-JAN-2001.
 XX PD 26-JUN-2000; 2000WO-EP005922.
 XX PF 25-JUN-1999; 99US-00344096.
 XX PR (UYZU-) UNIV ZUERICH.
 XX PA Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX PI WPI; 2001-137954/14.
 XX DR Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX Claim 6; Page 40; 56pp; English.
 XX The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for

CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX Sequence 32 AA;
 SQ
 Query Match 54.5%; Score 6; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DENVAL 9
 Db 13 DENVAL 18
 RESULT 11
 AAB61571
 ID AAB61571 standard; peptide; 37 AA.
 XX AC AAB61571;
 XX 03-APR-2001 (first entry)
 DT Peptide Winzip-B1 used to identify hetero-associating peptides.
 DE Hetero-associating coiled-coil peptide; heterodimerisation.
 XX KW Unidentified.
 XX OS WO200100814-A2.
 XX PN 04-JAN-2001.
 XX PD 26-JUN-2000; 2000WO-EP005922.
 XX PF 25-JUN-1999; 99US-00344096.
 XX PR (UYZU-) UNIV ZUERICH.
 XX PA Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX PI WPI; 2001-137954/14.
 XX DR Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX Example 3; Page 27; 56pp; English.
 XX The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX Sequence 37 AA;
 SQ
 Query Match 54.5%; Score 6; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DENVAL 9

```

Db      16 DENVAL 21
|||||
RESULT 12
AAG88621
ID AAG88621 standard; peptide; 9 AA.
AC AAG88621;
XX
XX 11-SEP-2001 (first entry)
XX
XX HER2/NEU DR supermotif binding peptide core sequence #167.
XX
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200141787-A1.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033591.
XX
XX 10-DEC-1999; 99US-00458299.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX Keogh E;
XX
XX WPI; 2001-374995/39.
XX
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
XX cellular immune responses for the prevention and treatment of cancer.
XX
XX Disclosure; Page 172; 199pp; English.
XX
XX The present invention describes isolated prepared HER2/neu epitopes (I).
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
XX culture in vitro and binds to a complex of an epitope (I), bound to a
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
XX and a second epitope and the peptide is less than 50 contiguous amino
XX acids that have 100% identity with a native peptide sequence of HER2/neu;
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
XX immunostimulant activities, and can be used in vaccines. (I), (II) and
XX (III) are useful for inducing cellular immune responses for the
XX prevention and treatment of cancer. (I) and (II) are useful for
XX monitoring or evaluating an immune response to a tumour-associated
XX antigen when incubated with a T lymphocyte sample from a patient and
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope
XX based vaccines mean that immunosuppressive epitopes that may be present
XX in whole antigens may be avoided. Selected epitopes may be combined to
XX enhance immunogenicity. The possible pathological side effects caused by
XX infectious agents or whole protein antigen is eliminated. The vaccine
XX provides the ability to direct and focus an immune response to multiple
XX selected antigens from the same pathogen. Epitope-based anti-tumour
XX vaccines provides the opportunity to combine epitopes derived from
XX multiple tumour-associated molecules addressing the problem of tumour-
XX tumour variability and reducing the likelihood of tumour escape due to
XX antigen loss. AAG89266 to AAG89121 represent amino acid sequences used in
XX the exemplification of the present invention
XX
XX Sequence 9 AA;
XX
XX Query Match 45.5%; Score 5; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Query Match 45.5%; Score 5; DB 4; Length 9;
Sequence 9 AA;

```

```

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYALA 10
Db 5 NYALA 9

RESULT 14
AAE31119
ID AAE31119 standard; peptide; 9 AA.
AC AAE31119;
XX
XX
DT 24-FEB-2003 (first entry)
XX
XX Human erb2 peptide #4.
XX
XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX
XX Homo sapiens.
XX
XX WO200272627-A2.
XX
XX 19-SEP-2002.
XX
XX 11-MAR-2002; 2002WO-EP002666.
XX
XX 09-MAR-2001; 2001US-0274250P.
XX
XX 14-MAY-2001; 2001US-0290353P.
XX
XX 18-MAY-2001; 2001US-0291610P.
XX
XX (CALL-) CALLISTOGEN AG.
XX
XX Wrede P, Walden P, Eichler-Mertens M, Filter M;
XX
XX WPI; 2002-759836/82.
XX
XX Providing, identifying or optimizing peptides for inducing cytotoxic T-
XX lymphocytes and for treating cancer, comprises selecting conserved
XX regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
XX protein.
XX
XX Disclosure; Page 7; 32pp; English.
XX
XX The invention relates to a method for providing, identifying or/and
XX optimizing peptides which induce cytotoxic T-lymphocytes and to the uses
XX of the obtained peptides for vaccination. The method is useful for
XX providing, identifying and/or optimising peptides that are useful in
XX manufacturing a pharmaceutical composition for the induction of cytotoxic
XX T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
XX or viral infections. The invention is also used in gene therapy. The
XX present sequence is human erb2 peptide used to illustrate the method of
XX the invention
XX
XX Sequence 9 AA;
Query Match 45.5%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYALA 10
Db 5 NYALA 9

RESULT 15
ADN64564
ID ADN64564 standard; peptide; 9 AA.
XX
XX AC ADN64564;
XX
XX 01-JUL-2004 (first entry)

```

```

XX HLA binding peptide #1164.
XX
XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
XX gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
XX prostate specific antigen; prostate specific membrane antigen;
XX hepatitis B virus antigen; hepatitis C virus antigen;
XX malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
XX prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
XX chondylooma acuminatum.
XX
XX Unidentified.
XX
XX WO2004031211-A2.
XX
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031308.
XX
XX 03-OCT-2002; 2002US-0416207P.
XX
XX 08-OCT-2002; 2002US-0417269P.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sidney J, Southwood S, Sette A;
XX
XX WPI; 2004-347953/32.
XX
XX New composition of peptides and nucleic acids capable of binding Major
XX Histocompatibility Complex molecules, useful for diagnosing, preventing
XX or treating viral infections or cancer, such as prostate cancer,
XX hepatitis B or AIDS.
XX
XX Claim 1; SEQ ID NO 1164; 186pp; English.
XX
XX The invention relates to a novel composition comprising one or more
XX peptides or nucleic acids encoding an HLA binding peptide. The
XX composition further comprises an HTL epitope. It also comprises a spacer
XX molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
XX are incorporated as part of a liposome. The peptide is from an antigen
XX selected from prostate specific antigen (PSA), prostate specific membrane
XX antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
XX antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
XX immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
XX Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
XX murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
XX (TKP). The composition is useful for preventing or treating viral
XX infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
XX AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondylooma
XX acuminatum. The composition is also be used for diagnosing such diseases.
XX This sequence represents a peptide of the invention.
XX
XX Sequence 9 AA;
Query Match 45.5%; Score 5; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYALA 10
Db 4 NYALA 8

Search completed: May 5, 2005, 18:18:05
Job time : 102.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds
(without alignments)
52.052 Million cell updates/sec

Title: US-10-827-133-9
Perfect score: 11
Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	8	I48935	apolipoprotein A-I
2	4	36.4	9	A33527	fructose-2,6-bisph
3	4	36.4	12	S11298	hemagglutinin prec
4	4	36.4	13	A38929	glutathione peroxi
5	4	36.4	14	QMWAVV	mastoparan - yello
6	4	36.4	15	A46586	hemoglobin (N-term
7	4	36.4	20	S68028	iodothronine 5'-mo
8	4	36.4	20	S19616	globin - polychaet
9	4	36.4	24	A47209	histone H-1-MDBP-2
10	4	36.4	27	A33210	protein disulfide-
11	4	36.4	27	PC4234	hypothetical prote
12	4	36.4	28	T14210	NADH2 dehydrogenas
13	4	36.4	28	E81239	hypothetical prote
14	4	36.4	30	I19799	CAT-66 - Bacillus
15	4	36.4	32	F60529	hemocyanin M1 - cr
16	4	36.4	33	FD15G	antifreeze protein
17	4	36.4	33	A05162	antifreeze protein
18	4	36.4	37	AH2787	hypothetical prote
19	4	36.4	38	B82413	hypothetical prote
20	4	36.4	39	A80930	probable bacteriop
21	4	36.4	39	AF0836	antifreeze protein
22	4	36.4	40	1 F018G	hypothetical prote
23	4	36.4	40	F81511	hypothetical prote
24	4	36.4	41	T35359	hypothetical prote
25	4	36.4	41	E24802	cuticle protein 32
26	4	36.4	42	1 WMBPPI	gene i protein - p
27	4	36.4	43	S35608	cytochrome P450 4A
28	4	36.4	44	2 B38075	N-acetylglactosam
29	4	36.4	44	2 S54144	tns1 protein - mou

30	4	36.4	45	2 A05163	antifreeze protein
31	4	36.4	46	1 ACBPT4	gene ac protein -
32	4	36.4	47	2 A56778	recombination prot
33	4	36.4	48	2 A56771	34K epidermal grow
34	4	36.4	48	2 A84368	hypothetical prote
35	4	36.4	48	2 S59076	hypothetical prote
36	4	36.4	49	2 PX0029	protein C inhibito
37	4	36.4	49	2 G44530	T-cell receptor al
38	4	36.4	50	2 D69287	hypothetical prote
39	4	36.4	50	2 C82690	hypothetical prote
40	3	27.3	4	2 S18401	thryoglobulin - do
41	3	27.3	5	2 S55237	zinc-binding prote
42	3	27.3	5	2 PT0281	Ig heavy chain CRD
43	3	27.3	5	2 A32014	tram protein - Esc
44	3	27.3	8	2 A37521	R-phycocerythrin ga
45	3	27.3	8	2 H41978	calliceramide 8 -

ALIGNMENTS

RESULT 1

I48935

apolipoprotein A-II - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48935

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5; 349-355, 1994

A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I48935

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-8 <RES>

A:Cross-references: UNIPROT:Q62528; EMBL:U05692; NID:G497011; PIDN:AAB60463.1; PID:G6428

Query Match 36.4%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 ALAA 11

Db 4 ALAA 7

RESULT 2

A33527

fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - rat (fragment)

N:Alternate names: fructose-2,6-bisphosphatase

C:Species: Rattus norvegicus (Norway rat)

C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jun-1993

C:Accession: A33527

R:Kitamura, K.; Uyeda, K.; Hartman, F.C.; Kangawa, K.; Matsuo, H.

J. Biol. Chem. 264, 6344-6348, 1989

A>Title: Catalytic site of rat liver and bovine heart fructose-6-phosphate,2-kinase:fruc

A:Reference number: A33527; MUID:89197937; PMID:2539378

A:Accession: A33527

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <KIT>

C:Keywords: phosphoric monoester hydrolase

Query Match 36.4%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 ALAA 11

Db 4 ALAA 7

RESULT 3

S11298
 hemagglutinin precursor - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)
 C;Species: influenza A virus
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
 C;Accession: S11298
 R;Robertson, J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A virus
 A;Reference number: S11286; MUID:80034428; PMID:493121
 A;Accession: S11298
 A;Molecule type: genomic RNA
 A;Residues: 1-12 <ROB>
 A;Cross-references: GB:J02111
 C;Genetics:
 A;Map position: segment 4
 C;Superfamily: Influenza virus hemagglutinin
 C;Keywords: homotrimer

Query Match 36.4%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 Db 9 ALAA 12

RESULT 4
 A38929
 glutathione peroxidase (EC 1.11.1.9) - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A38929
 R;Gettins, P.; Dyal, D.; Crews, B.
 Arch. Biochem. Biophys. 294, 511-518, 1992
 A;Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes
 A;Reference number: S21712; MUID:92231574; PMID:1567207
 A;Accession: A38929
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <GET>
 A;Cross-references: UNIPROT:Q7M355
 C;Superfamily: glutathione peroxidase
 C;Keywords: oxidoreductase

Query Match 36.4%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 Db 4 ALAA 7

RESULT 5
 QMWAUV
 mastoparan - yellowjacket (Vespula lewisii)
 C;Species: Vespula lewisii
 C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
 C;Accession: A01776
 R;Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, C.
 Chem. Pharm. Bull. 27, 1942-1944, 1979
 A;Title: A new mast cell degranulating peptide mastoparan in the venom of Vespula-lewisii
 A;Reference number: S21776; MUID:80155337; PMID:540362
 A;Accession: A01776
 A;Molecule type: protein
 A;Residues: 1-14 <HIP>
 A;Cross-references: UNIPROT:P01514
 A;Note: The active peptide was also synthesized
 C;Comment: This cytotoxic peptide from wasp venom induces mast cell degranulation. The
 C;Superfamily: mastoparan
 C;Keywords: amidated carboxyl end
 F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 36.4%; Score 4; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 Db 5 ALAA 8

RESULT 6
 A46586
 hemoglobin (N-terminal, linker chain L2) - earthworm (Lumbricus terrestris) (fragment)
 C;Species: Lumbricus terrestris (Common earthworm)
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A46586
 R;Omby, D.W.; Zhu, H.; Schneider, K.; Beavis, R.C.; Chait, B.T.; Riggs, A.F.
 J. Biol. Chem. 268, 13539-13547, 1993
 A;Title: The extracellular hemoglobin of the earthworm, Lumbricus terrestris. Determination of the amino acid sequence
 A;Reference number: A46586; MUID:93293879; PMID:8514787
 A;Accession: A46586
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <OWN>
 A;Cross-references: UNIPROT:Q9TWT5
 A;Note: sequence extracted from NCBI backbone (NCBIP:134509)

Query Match 36.4%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 Db 9 ALAA 12

RESULT 7
 S68028
 iodothronine 5'-monodeiodinase - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S68028
 R;Zhou, L.X.; Dehal, S.S.; Kupfer, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., E.D.;
 Arch. Biochem. Biophys. 322, 390-394, 1995
 A;Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, microsomal
 A;Reference number: S68028; MUID:96032659; PMID:7574712
 A;Accession: S68028
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <ZHO>
 C;Superfamily: protein disulfide-isomerase; thioredoxin homology

Query Match 36.4%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 Db 12 ALAA 15

RESULT 8
 S19616
 globin - polychaete (Eudistylia vancouveri) (fragment)
 N;Alternate names: chlorocruzin
 C;Species: Eudistylia vancouveri
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C;Accession: S19616
 R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.
 J. Mol. Biol. 222, 1109-1129, 1991
 A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular chain
 A;Reference number: S19532; MUID:92106333; PMID:1762147

A:Accession: S19616
 A:Molecule type: protein
 A:Residues: 1-20 <QAB>
 C:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodecamer; calcium; dodecamer; heme; homotetramer; oxygen carrier
 C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 36.4%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALA 10
 ||||
 DB 10 YALA 13

RESULT 9
 A47209
 histone H-1-MDBP-2 - chicken (fragments)
 C:Species: Gallus gallus (chicken)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 27-Jun-1994
 C:Accession: A47209
 R:Jost, J.P.; Hofsteenge, J.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9499-9503, 1992
 A:Title: The repressor MDBP-2 is a member of the histone H1 family that binds preferentially to nucleosomes
 A:Reference number: A47209; PMID:93028489; PMID:1409659
 A:Accession: A47209
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <JOS>

Query Match 36.4%; Score 4; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 DB 14 ALAA 17

RESULT 10
 A33210
 protein disulfide-isomerase (EC 5.3.4.1), pancreatic - dog (fragment)
 N:Alternate names: S-S rearrangase
 C:Species: Canis lupus familiaris (dog)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 12-Apr-1995
 C:Accession: A33210
 R:Michalak, M.
 submitted to the Protein Sequence Database, July 1991
 A:Reference number: A33210
 A:Accession: A33210
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-27 <MIC>
 C:Superfamily: protein disulfide-isomerase; thioredoxin homology
 C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 36.4%; Score 4; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 DB 20 ALAA 23

RESULT 11
 PC4234
 hypothetical protein 27 - Synecococcus sp. (fragment)
 C:Species: Synecococcus sp.
 C:Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C:Accession: PC4234
 R:Fujishiro, T.; Kaneko, T.; Sugiyama, M.; Sugita, M.
 DNA Res. 3, 165-169, 1996

A:Title: Organization and transcription of a putative gene cluster encoding ribosomal proteins
 A:Reference number: JC5120; PMID:97061204; PMID:8905234
 A:Accession: PC4234
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-27 <FUG>
 A:Cross-references: UNIPROT:Q55018; DBJ: D85103
 A:Experimental source: strain PCC6301

Query Match 36.4%; Score 4; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 ||||
 DB 10 ALAA 13

RESULT 12
 T14210
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastix acanthinurus mitochondrion
 C:Species: mitochondrion Uromastix acanthinurus
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T14210
 R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Pang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A:Title: Two novel gene orders and the role of light-strand replication in rearrangement of mitochondrial DNA
 A:Reference number: 217789; PMID:97153826; PMID:9000757
 A:Accession: T14210
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-28 <MAC>
 A:Cross-references: UNIPROT:P92760; EMBL:U71325; NID:G1753264; PID:G1753265; PIDN:AA6522
 A:Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, University of Kansas
 C:Genetics:
 A:Genome: mitochondrion
 A:Note: ND1
 C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[N1Fe]-hydrogenase-3-t
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
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 DB 19 ALAA 22

RESULT 13
 E81239
 hypothetical protein NMB0093 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: E81239
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; PMID:20175755; PMID:10710307
 A:Accession: E81239
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-28 <TET>
 A:Cross-references: UNIPROT:Q9K1L8; GB:AE002368; GB:AE002098; NID:G7225303; PIDN:AAF4055
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0093

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDEN 6
||||
Db 3 NDEN 6

RESULT 14

I39799
CAT-66 - Bacillus pumilus (fragment)
C:Species: Bacillus pumilus
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39799
R:Duval, E.J.; Williams, D.M.; Mongkolsuk, S.; Lovett, P.S.
J. Bacteriol. 158, 784-790, 1984
A:Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
A:Reference number: I39799; MUID:84212298; PMID:6327638
A:Accession: I39799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: UNIPROT:Q45356; GB:K01811; NID:gl42647; PIDN:AAA22292.1; PID:g551698
C:Superfamily: chloramphenicol acetyltransferase

Query Match 36.4%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENY 7
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Db 6 DENY 9

RESULT 15

F60529
hemocyanin M1 - crayfish (Cherax destructor) (fragment)
C:Species: Cherax destructor (yabby)
C:Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 11-May-2000
C:Accession: F60529
R:Neuteboom, B.; Sierdsema, S.J.; Beintema, J.J.
Comp. Biochem. Physiol. B 94, 587-592, 1989
A:Title: The relationship between N-terminal sequences and immunological characterization
A:Reference number: A60529; MUID:90151075; PMID:2620501
A:Accession: F60529
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-32 <NEU>

Query Match 36.4%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDEN 6
||||
Db 27 NDEN 30

Search completed: May 5, 2005, 18:25:30
Job time : 22.3333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:09:44 ; Search time 28 Seconds
(without alignments)
29.326 Million cell updates/sec

Title: US-10-827-133-10
Perfect score: 11
Sequence: 1 AANDENYAASV 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
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5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	72.7	11	3	US-09-056-105-33
2	8	72.7	11	3	US-09-425-585-1
3	8	72.7	11	4	US-09-953-321-1
4	8	72.7	11	4	US-08-756-416-1
5	5	45.5	11	2	US-08-479-614-14
6	5	45.5	41	4	US-09-493-795B-316
7	4	36.4	4	6	5215909-6
8	4	36.4	4	6	5215909-6
9	4	36.4	4	6	5217869-73
10	4	36.4	5	6	5217869-73
11	4	36.4	7	3	US-07-994-133-7
12	4	36.4	6	1	US-09-060-726A-11
13	4	36.4	7	3	US-09-190-964-16
14	4	36.4	4	7	US-09-845-849A-11
15	4	36.4	8	3	US-08-688-988-48
16	4	36.4	9	1	US-08-178-570-74
17	4	36.4	9	3	US-08-369-643-74
18	4	36.4	9	3	US-09-133-062D-17
19	4	36.4	9	5	PCR-US95-00147-74
20	4	36.4	10	1	US-08-218-025A-169
21	4	36.4	10	2	US-08-518-967-8
22	4	36.4	12	1	US-08-405-200-16
23	4	36.4	12	3	US-08-596-257A-5
24	4	36.4	12	3	US-08-860-339-5
25	4	36.4	12	4	US-09-370-644B-5
26	4	36.4	12	4	US-09-573-629-5
27	4	36.4	12	4	US-10-208-349-5

28	4	36.4	13	2	US-08-162-149-5	Sequence 5, Appli
29	4	36.4	13	2	US-08-637-759B-193	Sequence 193, App
30	4	36.4	13	3	US-08-871-355A-193	Sequence 193, App
31	4	36.4	13	3	US-09-201-945-193	Sequence 193, App
32	4	36.4	13	5	PCT-US95-04121-26	Sequence 26, Appl
33	4	36.4	13	5	PCT-US95-04121-27	Sequence 27, Appl
34	4	36.4	13	5	PCT-US95-04121-28	Sequence 28, Appl
35	4	36.4	13	5	PCT-US95-04121-29	Sequence 29, Appl
36	4	36.4	13	5	PCT-US95-04121-30	Sequence 30, Appl
37	4	36.4	14	2	US-08-564-972-64	Sequence 64, Appl
38	4	36.4	15	1	US-08-408-604A-140	Sequence 140, App
39	4	36.4	15	2	US-08-553-257A-3	Sequence 3, Appli
40	4	36.4	15	3	US-09-140-201-14	Sequence 14, Appl
41	4	36.4	15	4	US-09-441-992-3	Sequence 3, Appli
42	4	36.4	15	5	PCT-US93-06751-87	Sequence 87, Appl
43	4	36.4	16	2	US-08-429-964-63	Sequence 63, Appl
44	4	36.4	16	4	US-09-009-953-24	Sequence 24, Appl
45	4	36.4	16	5	PCT-US93-08062-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-056-105-33
; Sequence 33, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: E.Coli
US-09-056-105-33

Query Match 72.7% Score 8; DB 3; Length 11;
Best Local Similarity 100.0%; Pred.No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8
| | | | |
Db 1 AANDENYA 8

RESULT 2

US-09-425-585-1
; Sequence 1, Application US/094255585
; Patent No. 6348315
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT

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; ORGANISM: Escherichia coli
US-09-425-585-1

Query Match      72.7%; Score 8; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
   |||||
Db 1 AANDENYA 8

RESULT 3
US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/953,321
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match      72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
   |||||
Db 1 AANDENYA 8

RESULT 4
US-08-756-416-1
; Sequence 1, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Fell, Perry
; APPLICANT: Mittler, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
; TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755
; FILING DATE: 30-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.41US01
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-756-416-1

Query Match      72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
   |||||
Db 1 AANDENYA 8

RESULT 5
US-08-479-614-14
; Sequence 14, Application US/08479614
; Patent No. 5861294
; GENERAL INFORMATION:
; APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N.,
; APPLICANT: Kerwin, Jr., James F., McNally, Teresa
; TITLE OF INVENTION: Adenosine Kinase Polypeptides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: D-377 AP6D, 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System 7.1
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,614
; FILING DATE: June 7, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5749.US.D1
; TELEPHONE: (708) 937-4884
; TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-479-614-14

Query Match 45.5%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
Db 4 YAASV 8

RESULT 6

US-09-493-795B-316
; Sequence 316, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-179.A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 316
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus catus
US-09-493-795B-316

Query Match 45.5%; Score 5; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDE 5
Db 7 AANDE 11

RESULT 7

US-09-493-795B-316
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:6;
; LENGTH: 4
US-09-493-795B-316

Query Match 36.4%; Score 4; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
Db 1 AASV 4

RESULT 8

5215909-6

; Patent No. 5215909

; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:6;
; LENGTH: 4
5215909-6

Query Match 36.4%; Score 4; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
Db 1 AASV 4

RESULT 9

5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73;
; LENGTH: 5
5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
Db 2 AAND 5

RESULT 10

5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73;
; LENGTH: 5
5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
Db 2 AAND 5

RESULT 11

US-07-994-133-7

; Sequence 7, Application US/07994133
; Patent No. 5436392
; GENERAL INFORMATION:
; APPLICANT: Thomas, John C.
; APPLICANT: Bohnert, Hans J.
; APPLICANT: Kanost, Michael R.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING M. SIXTA
; TITLE OF INVENTION: PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,133
; FILING DATE: 19921221
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenlee, Lorraine L.
; REGISTRATION NUMBER: 27,894
; REFERENCE/DOCKET NUMBER: 48-92
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; TELEX: 823189
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-994-133-7

Query Match 36.4%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 1 AASV 4

RESULT 12
US-09-060-726A-11
; Sequence 11, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-060-726A-11

Query Match 36.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 AASV 11
Db 1 AASV 4
RESULT 13
US-09-190-964-16
; Sequence 16, Application US/09190964
; Patent No. 6228989
; GENERAL INFORMATION:
; APPLICANT: Traugh, Jolinda A.
; APPLICANT: Tuzson, Polysena T.
; TITLE OF INVENTION: Peptide Substrates Phosphorylated By P21-Activated
; TITLE OF INVENTION: Protein Kinase
; FILE REFERENCE: 1279-276/988425
; CURRENT APPLICATION NUMBER: US/09/190,964
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-190-964-16

Query Match 36.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 3 AASV 6

RESULT 14
US-09-845-849A-11
; Sequence 11, Application US/09845849A
; Patent No. 6713663
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, Detlef
; APPLICANT: KARDAILSKY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026DV1
; CURRENT APPLICATION NUMBER: US/09/845,849A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-845-849A-11

Query Match 36.4%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 1 AASV 4

RESULT 15
US-08-688-988-48
; Sequence 48, Application US/08688988B

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; Patent No. 6096545
; GENERAL INFORMATION:
; APPLICANT: Lefebvre, Daniel D.
; APPLICANT: Malboobi, Mohammad A.
; TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
; FILE REFERENCE: PPL96-03
; CURRENT APPLICATION NUMBER: US/08/688,988B
; CURRENT FILING DATE: 1996-07-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
US-08-688-988-48
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Query Match      36.4%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ANDE 5
      |||
Db      4 ANDE 7
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Search completed: May 5, 2005, 18:24:19
Job time : 29 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:18:20 ; Search time 78 Seconds
(without alignments)
47.046 Million cell updates/sec

Title: US-10-827-133-10

Perfect score: 11

Sequence: 1 AANDENYAASV 11

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1428581 seqs, 333598853 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425092

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Post-processing: Listing first 45 summaries

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	72.7	11	9	US-09-953-321-1
2	8	72.7	11	9	US-09-975-132A-3
3	8	72.7	11	14	US-10-289-135A-119
4	8	72.7	12	14	US-10-080-866-19
5	6	54.5	16	14	US-10-037-243-3
6	5	45.5	16	14	US-10-031-874A-107
7	5	45.5	16	14	US-10-031-874A-108
8	5	45.5	17	14	US-10-031-874A-114
9	5	45.5	17	14	US-10-031-874A-159
10	5	45.5	19	10	US-09-977-797A-96
11	5	45.5	19	14	US-10-026-525-5
12	5	45.5	19	15	US-10-425-855-5
13	5	45.5	41	17	US-10-895-372-316

14	5	45.5	46	15	US-10-424-599-211029	Sequence 211029,
15	5	45.5	48	15	US-10-424-599-250324	Sequence 250324,
16	4	36.4	4	15	US-10-427-208-17	Sequence 17, Appl
17	4	36.4	7	9	US-09-291-809C-11	Sequence 11, Appl
18	4	36.4	7	9	US-09-845-849-11	Sequence 11, Appl
19	4	36.4	7	10	US-09-827-542-16	Sequence 16, Appl
20	4	36.4	8	13	US-10-007-761-30	Sequence 30, Appl
21	4	36.4	9	17	US-10-930-300-30	Sequence 30, Appl
22	4	36.4	10	9	US-09-997-267-5	Sequence 5, Appl
23	4	36.4	10	10	US-09-572-404B-295	Sequence 295, App
24	4	36.4	10	10	US-09-572-404B-1135	Sequence 1135, Ap
25	4	36.4	10	10	US-09-572-270A-35	Sequence 35, Appl
26	4	36.4	10	10	US-09-572-270A-37	Sequence 37, Appl
27	4	36.4	10	10	US-09-573-822C-230	Sequence 230, App
28	4	36.4	10	14	US-10-080-013-38	Sequence 38, Appl
29	4	36.4	10	15	US-10-430-685-231	Sequence 231, App
30	4	36.4	10	15	US-10-289-566-38	Sequence 38, Appl
31	4	36.4	12	9	US-09-753-126-141	Sequence 141, App
32	4	36.4	12	10	US-09-896-896A-105	Sequence 105, App
33	4	36.4	12	14	US-10-032-818-59	Sequence 59, Appl
34	4	36.4	12	14	US-10-286-457-19	Sequence 19, Appl
35	4	36.4	12	14	US-10-286-457-188	Sequence 188, App
36	4	36.4	12	14	US-10-286-457-679	Sequence 679, App
37	4	36.4	12	14	US-10-208-349-5	Sequence 5, Appl
38	4	36.4	12	15	US-10-330-697-141	Sequence 141, App
39	4	36.4	13	15	US-10-256-850-46	Sequence 46, Appl
40	4	36.4	13	14	US-10-014-340-785	Sequence 785, App
41	4	36.4	15	16	US-10-408-765A-3037	Sequence 3037, Ap
42	4	36.4	16	13	US-10-103-395-24	Sequence 24, Appl
43	4	36.4	16	14	US-10-082-014-154	Sequence 154, App
44	4	36.4	16	14	US-10-031-874A-164	Sequence 164, App
45	4	36.4	16	14	US-10-372-076-184	Sequence 184, App

ALIGNMENTS

RESULT 1

US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: PLOCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953.321
; PRIOR FILING DATE: 2001-09-14
; CURRENT FILING DATE: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match 72.7%; Score 8; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8

DB 1 AANDENYA 8

RESULT 2

US-09-975-132A-3
; Sequence 3, Application US/09975132A
; Publication No. US20020182672A1

; GENERAL INFORMATION:
; APPLICANT: Kolkman, Marc
; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a
; TITLE OF INVENTION: Microorganism
; FILE REFERENCE: GC636-2
; CURRENT APPLICATION NUMBER: US/09/975,132A
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/239,531
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide tag
US-09-975-132A-3

Query Match 72.7%; Score 8; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8
DB 1 AANDENYA 8

RESULT 3
US-10-289-135A-119
; Sequence 119, Application US/10289135A
; Publication No. US20030180937A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIU, GEORGE
; APPLICANT: DELISA, MATTHEW
; TITLE OF INVENTION: ENGINEERING OF LEADER PEPTIDES FOR THE SECRETION OF
; TITLE OF INVENTION: RECOMBINANT PROTEINS IN BACTERIA
; FILE REFERENCE: CLFR-019US
; CURRENT APPLICATION NUMBER: US/10/289,135A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/337,452
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-289-135A-119

Query Match 72.7%; Score 8; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8
DB 1 AANDENYA 8

RESULT 4
US-10-080-866-19
; Sequence 19, Application US/10080866
; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Paegle, E. Sasha
; APPLICANT: Reilly, Dorothée
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1732R1
; CURRENT APPLICATION NUMBER: US/10/080,866

; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/274,384
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide for generating antibodies
US-10-080-866-19

Query Match 72.7%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8
DB 2 AANDENYA 9

RESULT 5
US-10-037-243-3
; Sequence 3, Application US/10037243
; Publication No. US20030134352A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, LLC.
; APPLICANT: Freimuth, Paul I
; APPLICANT: Zhang, Yian-Biao
; APPLICANT: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
; FILE REFERENCE: BSA 01-22
; CURRENT APPLICATION NUMBER: US/10/037,243
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
US-10-037-243-3

Query Match 54.5%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDEN 6
DB 1 AANDEN 6

RESULT 6
US-10-031-874A-107
; Sequence 107, Application US/10031874A
; Publication No. US20030190596A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 16
; TYPE: PRT

; ORGANISM: Lama glama
US-10-031-874A-107

Query Match 45.5%; Score 5; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAASV 11
Db 10 YAASV 14
|||||

RESULT 7

US-10-031-874A-108
; Sequence 108, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-108

Query Match 45.5%; Score 5; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAASV 11
Db 10 YAASV 14
|||||

RESULT 8

US-10-031-874A-114
; Sequence 114, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-114

Query Match 45.5%; Score 5; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAASV 11
Db 10 YAASV 14
|||||

Db 11 YAASV 15

RESULT 9

US-10-031-874A-159
; Sequence 159, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-159

Query Match 45.5%; Score 5; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAASV 11
Db 11 YAASV 15
|||||

RESULT 10

US-09-977-797A-96
; Sequence 96, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-96

Query Match 45.5%; Score 5; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAASV 11
Db 13 YAASV 17
|||||

RESULT 11

US-10-026-925-5
; Sequence 5, Application US/10026925
; Publication No. US20030119056A1
; GENERAL INFORMATION:

; APPLICANT: LADNER, ROBERT C.
; TITLE OF INVENTION: FOCUSED LIBRARIES OF GENETIC PACKAGES
; FILE REFERENCE: DYAX/004
; CURRENT APPLICATION NUMBER: US/10/026,925
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
; OTHER INFORMATION: CDR2 vector
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Any amino acid except Cys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Any amino acid except Cys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-(7)
; OTHER INFORMATION: Any amino acid except Cys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Any amino acid except Cys
; OTHER INFORMATION: Any amino acid except Cys

US-10-026-925-5
Query Match 45.5%; Score 5; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
DB 13 YAASV 17

RESULT 12
US-10-855-5
; Sequence 5, Application US/10425855
; Publication No. US20040005324A1
; GENERAL INFORMATION:
; APPLICANT: PILKINGTON, GLENN
; APPLICANT: CHANOCK, ROBERT
; APPLICANT: CROWE, JAMES
; APPLICANT: MURPHY, BRIAN
; TITLE OF INVENTION: NEUTRALIZING MONOCLONAL ANTIBODIES TO RESPIRATORY
; FILE REFERENCE: 18602.0007/P007-A
; CURRENT APPLICATION NUMBER: US/10/425,855
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/043,530
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: 60/003,931
; PRIOR FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-855-5

Query Match 45.5%; Score 5; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11

DB 13 YAASV 17

RESULT 13
US-10-895-372-316
; Sequence 316, Application US/10895372
; Publication No. US20050032705A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hilliard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-286
; CURRENT APPLICATION NUMBER: US/10/895,372
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: US 09/493,795
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 316
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus catus
US-10-895-372-316

Query Match 45.5%; Score 5; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDE 5
DB 7 AANDE 11

RESULT 14
US-10-424-599-211029
; Sequence 211029, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 211029
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32586C.1.pep
US-10-424-599-211029

Query Match 45.5%; Score 5; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAS 10
DB 13 NYAAS 17

RESULT 15
US-10-424-599-250324

; Sequence: 250324, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250324
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68070C.1.pap
US-10-424-599-250324

Query Match 45.5%; Score 5; DB 15; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAVS 11
|||
Db 38 YAAVS 42

Search completed: May 5, 2005, 18:31:05
Job time : 79 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:00:34 ; Search time 101.333 Seconds
(without alignments)
41.984 Million cell updates/sec

Title: US-10-827-133-10

Perfect score: 11

Sequence: 1 AANDENYAASV 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	11	2	ABB84403
2	8	72.7	11	6	AAO16101
3	8	72.7	11	7	ADe48279
4	8	72.7	11	7	ADP50155
5	8	72.7	12	5	AAE28994
6	6	54.5	16	7	ADL33753
7	5	45.5	11	2	AAW08376
8	5	45.5	11	2	AAW73649
9	5	45.5	16	5	AAU82541
10	5	45.5	16	5	AAU82542
11	5	45.5	17	5	AAU82548
12	5	45.5	17	5	AAU82594
13	5	45.5	18	5	ABP62282
14	5	45.5	19	2	AAW16584
15	5	45.5	19	2	AAV05048
16	5	45.5	19	6	ABP56777
17	5	45.5	19	7	ADC82814
18	5	45.5	22	7	ADC33576
19	5	45.5	32	4	AAE1562
20	5	45.5	32	4	AAE1569
21	5	45.5	32	4	AAE1568
22	5	45.5	32	4	AAE1559
23	5	45.5	37	4	AAE1571
24	5	45.5	41	3	AAE21594
25	5	45.5	49	2	AAV11212

26	5	45.5	49	3	AAE40565	Aag40565 Arabidops
27	4	36.4	4	2	AAE55338	Aar55338 Inhibitor
28	4	36.4	5	2	AAE12715	Aar12715 Pentapept
29	4	36.4	5	2	AAE51579	Aar51579 Mimotope
30	4	36.4	5	2	AAE69947	Aar69947 Pentameri
31	4	36.4	5	2	AAE98693	Aar98693 Peptide 7
32	4	36.4	7	2	AAE66141	Aar66141 CD-4 anti
33	4	36.4	7	4	AAU03794	Aau03794 P21-activ
34	4	36.4	7	5	AAE49635	Aae49635 Human bet
35	4	36.4	7	6	AAE31849	Aae31849 Androgen
36	4	36.4	7	6	ADB17038	Adb17038 Peptide 8
37	4	36.4	8	4	ABE55811	ABe55811 Vascular
38	4	36.4	8	5	ABG31178	ABg31178 Rat delta
39	4	36.4	8	5	ABG78786	ABg78786 Multiple
40	4	36.4	9	2	AAW21230	AAW21230 Farnesyl
41	4	36.4	9	2	AAE79717	AAE79717 pp92(c-fp
42	4	36.4	9	3	AAE67918	AAE67918 P110gag-f
43	4	36.4	9	3	AAE03501	AAE03501 Human tyr
44	4	36.4	9	3	AAE03481	AAE03481 Human tyr
45	4	36.4	9	4	AAU06411	Aau06411 Human Leu

ALIGNMENTS

RESULT 1
ABB84403
ID ABB84403 standard; peptide; 11 AA.
XX
AC ABB84403;
XX
DT 21-OCT-2002 (first entry)
XX
DE B. coli derived aberrant protein C-terminal peptide motif.
XX
KW Tumour antigen; murine; vaccine; cellular immune response; immunogen;
KW cancer; tumour.
XX
OS Escherichia coli.
XX
FN US287569-B1.
XX
PD 11-SEP-2001.
XX
PF 06-APR-1998; 98US-00056105.
XX
PR 10-APR-1997; 97US-0043467P.
XX
(REGC) UNIV CALIFORNIA.
XX
Kipps TJ, Wu Y;
XX
WPI; 1998-583198/49.
XX
Generating cellular immune response in patient to target protein -
comprises introducing vector with nucleotide sequence encoding immunogen
comprising protein processing signal into cell of patient.
XX
Example 5; Col 6; 61pp; English.

This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents an E. coli aberrant protein motif described in the method of the invention. Note: The information in this spec has been previously disclosed in WO199845444 however this spec

```
CC contained no sequence information
XX
SQ Sequence 11 AA;

Query Match          72.7%; Score 8; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8
|||||

RESULT 2
AAO16101
ID AAO16101 standard; peptide; 11 AA.
XX
AC AAO16101;
XX
DT 27-FEB-2003 (first entry)
XX
DE C-terminal tag peptide.
XX
KW Gene therapy; vaccine; humoral immune response; cellular immune response;
KW immune response modulation; pathogenic infection; rheumatoid arthritis.
XX
OS Unidentified.
XX
PN WO200283181-A1.
XX
PD 24-OCT-2002.
XX
PF 18-APR-2002; 2002WO-AU000486.
XX
PR 18-APR-2001; 2001AU-00004468.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
WPI; 2003-075509/07.
XX
New compositions having antigens, polynucleotides encoding the antigens,
PT or antigen-presenting cells, useful for modulating an immune response,
PT e.g. for treating or preventing pathogenic infections or rheumatoid
PT arthritis.
XX
PS Disclosure; Page 35; 139pp; English.
XX
The invention comprises compositions for eliciting a humoral or cellular
CC immune response against a target antigen. The compositions of the
CC invention are useful for eliciting a humoral and cellular immune response
CC against a target antigen, modulating an immune response in a patient, and
CC the treatment or prophylaxis of a disease or condition. This includes
CC pathogenic infections (e.g. viral, bacterial, fungal or protozoan), or an
CC immune response to an autoantigen (e.g. rheumatoid arthritis). The
CC present amino acid sequence represents a peptide which was used in the
CC invention
XX
SQ Sequence 11 AA;

Query Match          72.7%; Score 8; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8
|||||

RESULT 3
ADE48279
ID ADE48279 standard; peptide; 11 AA.
XX
```

```
XX
AC ADE48279;
XX
DT 29-JAN-2004 (first entry)
XX
DE TAT dependant secretion clone #1.
XX
KW leader peptide; Twin Arginine Translocation pathway;
KW putative TAT leader peptide sequence.
XX
OS Synthetic.
XX
PN WO2003040335-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035618.
XX
PR 05-NOV-2001; 2001US-0337452P.
XX
PR 21-AUG-2002; 2002US-0337452P.
XX
PA (PERE-) RES DEV FOUND.
XX
PI Georgiou G, Delisa M;
XX
WPI; 2003-449453/42.
XX
Identifying a leader peptide that directs increased protein export in
PT bacteria by screening libraries of leader peptides for sequences that
PT allow rapid export and can rescue short-lived reporter protein from
PT degradation in cytoplasm.
XX
Example 7; SEQ ID NO 119; 63pp; English.
XX
The present sequence relates to identifying a leader peptide that directs
CC increased protein export in bacteria, optionally through the Twin
CC Arginine Translocation pathway, comprises screening of libraries of
CC putative leader peptides or their mutants for sequences that allow rapid
CC export and, thus, can rescue a short-lived reporter protein from
CC degradation in the cytoplasm. The method is useful in engineering of
CC leader peptides for the secretion of recombinant proteins in bacteria.
CC The leader peptides can be used to direct or enhance protein secretion.
CC The present sequence represents a putative TAT leader peptide sequence of
CC the invention.
XX
SQ Sequence 11 AA;

Query Match          72.7%; Score 8; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8
|||||

RESULT 4
ADF50155
ID ADF50155 standard; peptide; 11 AA.
XX
AC ADF50155;
XX
DT 12-FEB-2004 (first entry)
XX
DE S. enteritidis protease C-terminal fragment.
XX
KW promoter; mutant; vaccine; Shine Dalgarno; probiotic bacteria;
KW regulatory gene; targeted optimisation.
XX
OS Salmonella enteritidis.
XX
PN WO2003070941-A2.
XX
```


PD 28-AUG-2003.
XX
XX PF 19-FEB-2003; 2003WO-EP001676.
XX
XX PR 19-FEB-2002; 2002US-0357103P.
XX PR 05-JUL-2002; 2002US-039477P.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX PI Bumann D;
XX
XX DR WPI; 2003-712619/57.
XX
XX PT New bacterial promoters active in vivo, useful in preparation of live,
XX PT recombinant vaccines, also mutated Shine-Dalgarno sequences for
XX PT modulating promoter activity.
XX
XX PS Disclosure; SEQ ID NO 2; 92pp; German.
XX
XX CC This invention describes novel active promoters described as 4.5G, A.8H,
XX CC 1f, 3g, 1c, 2a, 4a, 10g, 12b, A.2A, A.7A, A.9D, A.10F, A.11B, A.11H,
XX CC A.12A, A.12G, CLII.4C, CLII.3A, CLII.9B, CLII.11C, CLII.12C, 3.2E, 3.4F,
XX CC 3.6B, 3.9A, 3.9E, A.11A, A.8.B, CLII.5A, 4.4G or A.1A and their mutants.
XX CC The invention also describes recombinant bacteria that contains the
XX CC promoter, operatively linked to a heterologous nucleic acid, live vaccine
XX CC containing the bacteria and constructs with mutations in the Shine
XX CC Dalgarno sequence. The target bacteria are those used as carriers in live
XX CC vaccines, particularly Salmonella or probiotic bacteria. The new
XX CC promoters are used in preparation of live vaccines, especially for
XX CC expression of heterologous antigen. Also the mutated Shine-Dalgarno
XX CC sequence is used to modify (especially reduce) the activity of regulatory
XX CC gene elements, for targeted optimisation of the properties of recombinant
XX CC live vaccines. The new promoters (and/or mutated Shine-Dalgarno
XX CC sequences) provide targeted modulation of gene expression, including,
XX CC where the promoter has high activity both in vivo and in vitro induction
XX CC of a two-phase immune response.
XX
XX SQ Sequence 11 AA;
Query Match 72.7%; Score 8; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;
QY 1 AANDENYA 8
|||||||
DB 1 AANDENYA 8
RESULT 5
AAE28994
ID AAE28994 standard; peptide; 12 AA.
XX
XX AC AAE28994;
XX
XX DT 27-JAN-2003 (first entry)
XX
XX DE Peptide used in the exemplification of the invention.
XX
XX KW Vector; prokaryotic cell.
XX
XX OS Unidentified.
XX
XX PN WO200272847-A2.
XX
XX PD 19-SEP-2002.
XX
XX PF 22-FEB-2002; 2002WO-US005069.
XX
XX PR 09-MAR-2001; 2001US-0274384P.
XX
XX PA (GETH) GENENTECH INC.
XX
XX PI Paegle ES, Reilly D, Yansura DG;

XX WPI; 2002-723363/78.
XX
XX PT New vector comprising anti-termination nucleic acid or RNA encoding the
XX PT polypeptide with a non-lambda promoter, useful for producing human
XX PT thrombopoietin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide.
XX
XX PS Example 2; Page 32; 70pp; English.
XX
XX CC The invention relates to vectors for producing a polypeptide heterologous
XX CC to prokaryotic cells and method for producing the polypeptide. The method
XX CC is useful for producing a polypeptide heterologous to prokaryotic cells.
XX CC The present sequence is a peptide used in the exemplification of the
XX CC invention
XX
XX SQ Sequence 12 AA;
Query Match 72.7%; Score 8; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.059; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;
QY 1 AANDENYA 8
|||||||
DB 2 AANDENYA 9
RESULT 6
ADL33753
ID ADL33753 standard; protein; 6 AA.
XX
XX AC ADL33753;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Bacteriophage T7 ssrA peptide.
XX
XX KW protein solubility; coxsackievirus and adenovirus receptor; CAR;
XX KW Bacteriophage T7; ssrA peptide.
XX
XX OS Enterobacteria phage T7.
XX
XX PN US2003134352-A1.
XX
XX PD 17-JUL-2003.
XX
XX PF 04-JAN-2002; 2002US-00037243.
XX
XX PR 04-JAN-2002; 2002US-00037243.
XX
XX PA (FREI/) FREIMUTH P I.
XX PA (ZHAN/) ZHANG Y.
XX PA (HOWI/) HOWITT J A.
XX
XX PI Freimuth PI, Zhang Y, Howitt JA;
XX
XX WPI; 2003-897262/82.
XX
XX DR Enhancing the solubility of, and promoting the adoption of native
XX PT conformation in a recombinantly expressed polypeptide comprises
XX PT expressing the polypeptide as a fusion protein with a charged N- or C-
XX PT terminal extension.
XX
XX PS Disclosure; Page 9; 21pp; English.
XX
XX CC The invention relates to a method of enhancing the solubility of, and
XX CC promoting the adoption of native protein conformation of a recombinantly
XX CC expressed polypeptide by expressing the polypeptide as a fusion protein
XX CC including a peptide extension with: net negative charge (not peptide T7A)
XX CC positioned at the carboxy terminus; or net charge +2 to -20, positioned
XX CC at the amino terminus. The nucleic acids encoding the polypeptide of
XX CC interest and the extension are fused and inserted into an expression
XX CC vector which is then introduced into a host cell in which the polypeptide
XX CC is produced. The polypeptide is especially one that is substantially

CC insoluble or inactive when expressed recombinantly without the peptide extension. The present sequence represents Bacteriophage T7 ssrA peptide, used in a fusion to demonstrate the method of the invention.

XX Sequence 6 AA;

Query Match 54.5%; Score 6; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AANDEN 6
| | | | |
Db 1 AANDEN 6

RESULT 7
AAW08376
ID AAW08376 standard; peptide; 11 AA.

XX AC AAW08376;

XX DT 30-MAR-1997 (first entry)

XX DE Rat brain adenosine kinase peptide 5.

XX KW Adenosine kinase; agonist; antagonist; monoclonal antibody.

XX OS Rattus sp.

XX PN WO9640937-A2.

XX PD 19-DEC-1996.

XX PF 31-MAY-1996; 96WO-US008097.

XX PR 07-JUN-1995; 95US-00480019.

XX PA (ABBO) ABBOTT LAB.

XX PI Cowart MD, Halbert DN, Kerwin JF, McNally T;

XX DR WPI; 1997-052334/05.

XX PT Rat brain, and human placenta short and long forms of adenosine kinase - used, e.g. for assaying for AK (antagonists or for prodn. of monoclonal antibodies against AK.

XX PS Disclosure; Fig 6a; 75pp; English.

XX CC Adenosine kinase (AK) (AAW08369) purified from rat brain was digested with endoprotease Arg C, and peptide fragments were separated by HPLC. 5 Peptides were sequenced (AAW08372-76). Internal portions of peptides 2 and 4 were used to design degenerate primers (see also AAT4846-47) that were utilised in the identification of rat brain DNA clones (see also CC AAT4843) coding for AK (AAW08369)

XX SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 YAA5V 11
| | | | |
Db 4 YAA5V 8

RESULT 8

AAW73649

ID AAW73649 standard; protein; 11 AA.

XX AC AAW73649;

XX XX

DT 23-MAR-1999 (first entry)
XX DE Rat adenosine kinase protein fragment.
XX KW Adenosine kinase; cytotoxic nucleoside resistance; anticancer; antiviral;
XX KW liver tumour; gout; acquired immune deficiency syndrome; tissue injury;
XX KW adenosine concentration; cytoprotection; rat.

OS Rattus sp.

XX PN US5861294-A.

XX PD 19-JAN-1999.

XX PF 07-JUN-1995; 95US-00479614.

XX PR 07-JUN-1995; 95US-00479614.

XX PA (ABBO) ABBOTT LAB.

XX PI Halbert DN, Kerwin JF, McNally T, Cowart MD;

XX DR WPI; 1999-130392/11.

XX PT New nucleic acid encoding adenosine kinases and related oligo-nucleotides - expression vectors and transformed cells, used to modulate adenosine levels and to screen for specific modulators.

XX PS Disclosure; Fig 6; 39pp; English.

XX CC This sequence is a fragment of the rat brain adenosine kinase (AK) of the invention. Cells transformed with the DNA are used to produce recombinant AK. The AK is used: (i) to screen for specific agonists and antagonists; (ii) to raise antibodies; and (iii) therapeutically (reduced levels of AK are associated with resistance to nucleoside analogues with cytotoxic, anticancer and antiviral properties, with liver tumours, gout and acquired immune deficiency syndrome). Fragments of the DNA sequence are used as primers and probes to screen DNA libraries and for identifying AK - encoding nucleic acid, also as antisense therapeutics (particularly to increase local adenosine concentrations at the site of tissue injury, increasing the level of cytoprotection)

XX SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 YAA5V 11
| | | | |
Db 4 YAA5V 8

RESULT 9

AAU82541

ID AAU82541 standard; peptide; 16 AA.

XX AC AAU82541;

XX DT 29-AUG-2003 (revised)

XX DT 23-APR-2002 (first entry)

XX DE Llama CDR2 region variable heavy chain fragment #34.

XX KW Llama; phage display library; variable heavy domain fragment; VHH; VH; sAb fragment; single domain anti-idiotypic antibody fragment;
XX KW phage display technology; immune system response; CDR1/H1; CDR2; CDR3; complementarity determining region.

XX OS Lama glama.

XX PN WO200190190-A2.

XX XX

PS Claim 16; Page 32; 46pp; English.

XX The present invention relates to a phage display library of variable
CC heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama
CC antibodies. The library is useful for in vitro selection against any
CC antigen of interest as a target. Single domain anti-idiotypic antibody
CC fragments are isolated from the library using phage display technology
CC and an antibody serving as an antigen. Such anti-idiotypic antibody
CC fragments have great potential in evoking the immune system response to
CC pathological antigens and in vaccine development. The large size of the
CC library considerably increases the probability of isolating from it
CC antigen-binding fragments having high affinity to almost any
CC predetermined target (antigen of interest). The library eliminates the
CC development of anti-idiotypic antibodies by immunisation and allows
CC isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the
CC llama heavy chain domain fragments of the invention. (Updated on 29-AUG-
XX 2003 to standardise OS field)

XX Sequence 17 AA;

Query Match 45.5%; Score 5; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAAVS 11
|
|
|
|
Db 11 YAAVS 15

RESULT 12

AAU82594
ID AAU82594 standard; peptide; 17 AA.

XX AC AAU82594;

XX 29-AUG-2003 (revised)

DT 23-APR-2002 (first entry)

DE Llama CDR2 region variable heavy chain fragment #48.

XX Llama; phage display library; variable heavy domain fragment; VHH; VH;
KW sdAb fragment; single domain anti-idiotypic antibody fragment;
KW phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
KW complementarity determining region.

XX Lama glama.

XX WO200190190-A2.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-CA000763.

XX 26-MAY-2000; 2000US-0207234P.

XX (CANA) NAT RES COUNCIL CANADA.

XX Tanha J, Dubuc G, Narang S;

XX WPI; 2002-083093/11.

XX New phage display library of variable heavy domain antigen-binding
PT fragments derived from llama antibodies, useful for in vitro selection
PT against any antigen of interest as a target.

XX Disclosure; Page 19a; 46pp; English.

XX The present invention relates to a phage display library of variable
CC heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama
CC antibodies. The library is useful for in vitro selection against any
CC antigen of interest as a target. Single domain anti-idiotypic antibody
CC fragments are isolated from the library using phage display technology
CC and an antibody serving as an antigen. Such anti-idiotypic antibody

CC fragments have great potential in evoking the immune system response to
CC pathological antigens and in vaccine development. The large size of the
CC library considerably increases the probability of isolating from it
CC antigen-binding fragments having high affinity to almost any
CC predetermined target (antigen of interest). The library eliminates the
CC development of anti-idiotypic antibodies by immunisation and allows
CC isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the
CC llama heavy chain domain fragments of the invention. (Updated on 29-AUG-
XX 2003 to standardise OS field)

XX Sequence 17 AA;

Query Match 45.5%; Score 5; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAAVS 11
|
|
|
|
Db 11 YAAVS 15

RESULT 13

ABP62282
ID ABP62282 standard; peptide; 18 AA.

XX AC ABP62282;

XX 10-OCT-2002 (first entry)

DE Human immunopeptide to HCV E2 glycoprotein heavy chain CDR #52.

XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.

XX Homo sapiens.

XX WO200259340-A1.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-US002303.

XX 26-JAN-2001; 2001US-0264451P.

XX (SCRI) SCRIPPS RES INST.

XX Maruyama T, Jones IM, Burton DR, Fox RI;

XX WPI; 2002-599801/64.

XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.

XX Claim 1; Fig 17; 308pp; English.

XX The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection

XX Sequence 18 AA;

Query Match 45.5%; Score 5; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
 |||||
 Db 12 YAASV 16

RESULT 14

AAW16584
 ID AAW16584 standard; peptide; 19 AA.

XX AC AAW16584;
 XX DT 30-NOV-1997 (first entry)
 XX DE Anti-RSV F glycoprotein antibody RSVF2-5 VH3 CDR2.
 XX KW Respiratory syncytial virus; RSV; monoclonal antibody; CDR;
 KW complementarity determining region; pneumonia; bronchiolitis; diagnosis;
 KW therapy; vaccine; RSVF2-5.
 XX OS Homo sapiens.
 XX PN WO9710846-A1.
 XX PD 27-MAR-1997.
 XX PF 18-SEP-1996; 96WO-US014937.
 XX PR 18-SEP-1995; 95US-0003931P.
 XX (INTR-) INTRACEL CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Pilkington GR, Gilmour PS, Chanock RM, Crowe JE, Murphy BR;
 DR WPI; 1997-202621/18.

XX Composition comprising respiratory syncytial virus antibody - useful for
 treatment or prophylaxis of active disease or infection.
 XX Claim 4; Page 48-49; 71pp; English.

XX This peptide sequence comprises complementarity determining region 2
 (CDR2) of the heavy chain VH3 sequence of a novel neutralising human
 monoclonal antibody to respiratory syncytial virus (RSV). The antibody,
 designated RSVF2-5 (ATCC 6909), selectively binds to an RSV F
 glycoprotein epitope. DNA encoding RSVF2-5 Fd and light chain (see
 AA166556-57) was isolated from a phage library prepared from the RNA of
 peripheral blood lymphocytes of an HIV-1 infected donor. A claimed
 pharmaceutical preparation comprises a carrier and an antibody that
 includes the RSVF2-5 VH3 CDR3 (AAW16586) and which may also include the
 VH3 CDR2 and/or CDR1 (AAW16582) or the entire Fd Fd region (AAW16580), or
 is an Fab fragment and further includes the RSVF2-5 VL6 CDR3 (AAW16594),
 CDR2 (AAW16592), CDR1 (AAW16590) or entire light chain (AAW16588). The
 preparation alternatively comprises a carrier and a vector that includes
 a nucleotide sequence encoding the antibody. The preparations can be used
 for the treatment or prophylaxis of active RSV disease or infection
 (claimed), and may also be used for RSV detection. The antibody binds and
 neutralises antigenic subgroups A and B of RSV with high efficiency

Sequence 19 AA;

Query Match 45.5%; Score 5; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
 |||||
 Db 13 YAASV 17

RESULT 15

AAV05048

ID AAV05048 standard; peptide; 19 AA.
 XX AAV05048;
 XX DT 16-JUN-1999 (first entry)
 XX DE Tumour antigen antibody heavy chain CDR2 clone F14.
 XX KW Tumour antigen; antibody; CDR; complementarity determining region;
 KW binding molecule identification; tumour-specific binding polypeptide;
 KW cancer therapy; heavy chain.
 XX OS Homo sapiens.
 XX PN WO9906834-A2.
 XX PD 11-FEB-1999.
 XX PF 04-AUG-1998; 98WO-US016280.
 XX PR 04-AUG-1997; 97US-00905825.
 XX (IXSY-) IXSYS INC.
 XX PI Watkins JD, Huse WD, Wu H;
 DR WPI; 1999-153951/13.
 DR N-PSDB; AAX28225.
 XX Identifying binding molecules for ligands, particularly tumour antigens -
 by selectively immobilising a population of binding molecules to a solid
 support and screening for binding to two or more ligands.
 XX Claim 15; Page 60; 80pp; English.

XX This sequence represents a heavy chain complementarity determining region
 (CDR) from a tumour antigen specific antibody. The invention relates to a
 method for identifying a binding molecule having selective affinity for a
 ligand comprising: (a) selectively immobilising a diverse population of
 binding molecules to a solid support; (b) simultaneously contacting the
 diverse population immobilised on the solid support with 2 or more
 ligands; and (c) determining at least one binding molecule which
 selectively binds to one or more of the ligands. The method allows for
 the rapid and efficient methods for the identification of binding
 molecules which exhibit selective affinity for one or more ligands of
 interest. They are used particularly for identifying tumour-specific
 binding polypeptides which can be used as targeting agents for cancer
 therapy that minimises impact on non-tumour tissues

Sequence 19 AA;

Query Match 45.5%; Score 5; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
 |||||
 Db 13 YAASV 17

Search completed: May 5, 2005, 18:18:07
 Job time : 103.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds
(without alignments)
52.052 Million cell updates/sec

Title: US-10-827-133-10

Perfect score: 11

Sequence: 1 AANDENYAASV 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	19	2 B61056	cytochrome P450 PB
2	4	36.4	20	2 S10680	probable 7-ethoxyc
3	4	36.4	22	2 B33174	sorbinin - sorghum
4	4	36.4	28	2 E81239	hypothetical prote
5	4	36.4	29	2 S10050	ribosomal protein
6	4	36.4	30	2 I39799	CAT-66 - Bacillus
7	4	36.4	30	2 S30333	N-carbamoyl-D-amin
8	4	36.4	32	2 F23454	ovalbumin phosphos
9	4	36.4	32	2 F60529	hemocyanin M1 - cr
10	4	36.4	33	2 E82553	hypothetical prote
11	4	36.4	34	2 A33564	neurogenic protein
12	4	36.4	35	2 S27307	surface-array prot
13	4	36.4	37	1 R5PM81	ribosomal protein
14	4	36.4	37	2 PC1121	antifungal 25K pro
15	4	36.4	37	2 AH2187	hypothetical prote
16	4	36.4	38	2 S22210	photosystem I prot
17	4	36.4	38	2 A32790	interferon gamma-1
18	4	36.4	38	2 T14226	NADH2 dehydrogenas
19	4	36.4	38	2 I48924	homeobox protein -
20	4	36.4	39	2 AB0930	hypothetical prote
21	4	36.4	39	2 AF0836	probable bacteriop
22	4	36.4	40	2 A57482	photosystem I prot
23	4	36.4	46	2 B45174	eye cell developme
24	4	36.4	48	2 A84368	hypothetical prote
25	4	36.4	49	2 G44530	T-cell receptor al
26	4	36.4	50	2 AC2028	hypothetical prote
27	3	27.3	5	2 PT0281	Ig heavy chain CRD
28	3	27.3	5	2 A32014	traw protein - Esc
29	3	27.3	6	2 PT0560	T-cell receptor be

30 3 27.3 8 2 H41978
31 3 27.3 8 2 A61467
32 3 27.3 8 2 S68325
33 3 27.3 9 2 PT0272
34 3 27.3 9 2 S10920
35 3 27.3 9 2 A45199
36 3 27.3 10 2 S15118
37 3 27.3 10 2 PN0136
38 3 27.3 10 2 A61354
39 3 27.3 11 2 S60294
40 3 27.3 12 2 A55837
41 3 27.3 12 2 C30503
42 3 27.3 12 2 C60529
43 3 27.3 13 2 A46463
44 3 27.3 14 2 PA0013
45 3 27.3 14 2 G44957

ALIGNMENTS

RESULT 1

B61056

Cytochrome P450 PB-B - chicken (fragment)

C:Species: Gallus gallus (Chicken)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: B61056

R:Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.

Comp. Biochem. Physiol. C 96: 163-176, 1990

A:Title: Purification and characterization of cytochrome P-450 isozymes from phenobarbi-

A:Reference number: A61056; MUID:91130218; PMID:1980873

A:Accession: B61056

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <GUP>

A:Cross-references: UNIPROT:Q7LZ30

Query Match 36.4%; Score 4; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11

DB 6 AASV 9

RESULT 2

S10680

Probable 7-ethoxycoumarin O-deethylase (EC 1.14.14.-) cytochrome P450 isoform 1 - chick

C:Species: Gallus gallus (chicken)

C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 16-Aug-2004

C:Accession: S10680

R:Sinclair, J.F.; Wood, S.; Lambrecht, L.; Gorman, N.; Mende-Mueller, L.; Smith, L.; Hu

Biochem. J. 269: 85-91, 1990

A:Title: Isolation of four forms of acetone-induced cytochrome P-450 in chicken liver by

A:Reference number: S10680; MUID:90328998; PMID:2375760

A:Accession: S10680

A:Molecule type: protein

A:Residues: 1-20 <SIN>

C:Superfamily: cytochrome P450 homology

C:Keywords: heme; membrane protein; microsome; monooxygenase; oxidoreductase

Query Match

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11

DB 6 AASV 9

RESULT 3

B33174

sormatin - sorghum (fragment)
 C;Species: Sorghum bicolor (sorghum)
 C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 09-Jul-2004
 C;Accession: B33174
 R;Vigers, A.J.; Roberts, W.K.; Selitrennikoff, C.P.
 submitted to the Protein Sequence Database, May 1991
 A;Reference number: A33174
 A;Accession: B33174
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <VIG>
 A;Cross-references: UNIPROT:Q9S908
 C;Superfamily: thaumatin I

Query Match 36.4%; Score 4; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
 ||||
 Db 15 AASV 18

RESULT 4
 E81239
 hypothetical protein NMB0093 [imported] - Neisseria meningitidis (strain MC58 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: E81239
 R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Nasigiani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: E81239
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <TE>
 A;Cross-references: UNIPROT:Q9KIL8; GB:AE002368; GB:AE002098; NID:G7225303; PIDN:AAF4055
 A;Experimental source: serogroup B, strain MC58
 C;GeneticS:
 A;Gene: NMB0093

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NDEN 6
 ||||
 Db 3 NDEN 6

RESULT 5
 S10050
 ribosomal protein L19.e - fission yeast (Schizosaccharomyces pombe) (fragment)
 N;Alternate names: ribosomal protein SP-L15
 C;Species: Schizosaccharomyces pombe
 C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C;Accession: S10050
 R;Otsuka, E.; Higo, K.I.; Itoh, T.
 Mol. Gen. Genet. 191, 519-524, 1983
 A;Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from Schizosaccha
 A;Reference number: S07293; MUID:84038947; PMID:6355773
 A;Accession: S10050
 A;Molecule type: protein
 A;Residues: 1-29 <OTA>
 A;Cross-references: UNIPROT:P05734
 C;Superfamily: rat ribosomal protein L19
 C;Keywords: protein biosynthesis; ribosome

Query Match 36.4%; Score 4; DB 2; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
 ||||
 Db 10 AASV 13

RESULT 6
 I39799
 CAT-66 - Bacillus pumilus (fragment)
 C;Species: Bacillus pumilus
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I39799
 R;Duval, E.J.; Williams, D.M.; Mongkolsuk, S.; Lovett, P.S.
 J. Bacteriol. 158, 784-790, 1984
 A;Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
 A;Reference number: I39799; MUID:84212298; PMID:6327638
 A;Accession: I39799
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-30 <RES>
 A;Cross-references: UNIPROT:Q45356; GB:K01811; NID:G142647; PIDN:AAA22292.1; PID:G551696
 C;Superfamily: chloramphenicol acetyltransferase

Query Match 36.4%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DENY 7
 ||||
 Db 6 DENY 9

RESULT 7
 S30333
 N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp. (fragment)
 C;Species: Comamonas sp.
 C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000
 C;Accession: S30333
 R;Ogawa, J.; Shimizu, S.; Yamada, H.
 Eur. J. Biochem. 212, 685-691, 1993
 A;Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c. Purification
 A;Reference number: S30333; MUID:93215645; PMID:8462543
 A;Accession: S30333
 A;Molecule type: protein
 A;Residues: 1-30 <OGA>
 A;Experimental source: strain E222c
 C;Function:
 A;Description: amidohydrolase with strict specificity for the D-form and strict substrat
 bamoyl-DL-aspartate
 C;Superfamily: hypothetical protein YLR351c
 C;Keywords: hydrolase

Query Match 36.4%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAA 9
 ||||
 Db 5 NYAA 8

RESULT 8
 F23454
 ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)
 C;Species: Dendrocygna bicolor (fulvous whistling-duck)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: F23454
 R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.
 Eur. J. Biochem. 114, 439-450, 1981
 A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.
 A;Reference number: A91106; MUID:81164535; PMID:6783411

A:Accession: F23454
 A:Molecule type: protein
 A:Residues: 1-32 <HEN>
 A:Cross-references: UNIPROT:Q7LZD7
 C:Superfamily: Serpin

Query Match 36.4%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
 ||||
 Db 24 AASV 27

RESULT 9

F60529
 hemocyanin M1 - crayfish (Cherax destructor) (fragment)
 C:Species: Cherax destructor (yabby)
 C:Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 11-May-2000
 A:Accession: F60529
 R:Neuteboom, B.; Sierdsema, S.J.; Beintema, J.J.
 Comp. Biochem. Physiol. B 94, 587-592, 1989
 A:Title: The relationship between N-terminal sequences and immunological characterization
 A:Reference number: A60529; MUID:90151075; PMID:2620501
 A:Accession: F60529
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-32 <NEU>

Query Match 36.4%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDEN 6
 ||||
 Db 27 NDEN 30

RESULT 10

E82553
 hypothetical protein XP2468 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 A:Accession: E82553
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82553; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: E82553
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-33 <SIM>

A:Cross-references: UNIPROT:Q9PAM8; GB:AE004055; GB:AE003849; NID:g9107661; PIDN:AAF8526
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tshunako, M.H.; Vallada, H.; da Silva, A.M.; Silva Jr., W.A.; da Silveira A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2468

Query Match 36.4%; Score 4; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
 ||||
 Db 7 AASV 10

RESULT 11

A43564
 neurogenic protein delta - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 A:Accession: A43564
 R:Haenlin, M.; Kramatschek, B.; Campos-Ortega, J.A.
 Development 110, 905-914, 1990
 A:Title: The pattern of transcription of the neurogenic gene Delta of Drosophila melanogaster
 A:Reference number: A43564; MUID:91209246; PMID:2128477
 A:Accession: A43564
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-34 <HAE>
 A:Cross-references: UNIPROT:Q95RM9
 C:Genetics:
 A:Gene: FlyBase:DL
 A:Cross-references: FlyBase:FBgn0000463
 C:Superfamily: neurogenic protein delta; EGF homology

Query Match 36.4%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
 ||||
 Db 10 AASV 13

RESULT 12

S27307
 surface-array protein - Aeromonas hydrophila (fragment)
 C:Species: Aeromonas hydrophila
 C:Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
 A:Accession: S27307; A33184
 R:Kokka, R.P.; Vedros, N.A.; Janda, J.M.
 J. Gen. Microbiol. 138, 1229-1236, 1992
 A:Title: Immunochemical analysis and possible biological role of an Aeromonas hydrophila
 A:Reference number: S27307; MUID:92407495; PMID:1382113
 A:Accession: S27307
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-35 <KO2>
 A:Cross-references: UNIPROT:Q9R5H9

Query Match 36.4%; Score 4; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
 ||||
 Db 6 AASV 9

RESULT 13

R5PM81
 ribosomal protein L36 - garden pea chloroplast
 C:Species: chloroplast Pisum sativum (garden pea)
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 A:Accession: A27301; S04382
 R:Purton, S.; Gray, J.C.
 Nucleic Acids Res. 15, 9080, 1987
 A:Title: Nucleotide sequence of the gene for ribosomal protein L36 in pea chloroplast
 A:Reference number: A27301; MUID:88067720; PMID:3684583

A;Accession: A27301
A;Molecule type: DNA
A;Residues: 1-37 <PUR>
A;Cross-references: UNIPROT:P07815; GB:Y00468; NID:gl2162; PIDN:CAA68531.1; PID:gl2163
C;Genetics:
A;Gene: xpl36
A;Genome: Chloroplast
C;Superfamily: Escherichia coli ribosomal protein L36
C;Keywords: chloroplast; protein biosynthesis; ribosome
F;1-37/Product: ribosomal protein L36a #status predicted <MAT>

Query Match 36.4%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 4 AASV 7

RESULT 14

PC1121
antifungal 25K protein - flax (fragment)
C;Species: Linum usitatissimum (flax)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1121
R;Borgmeyer, J.R.; Smith, C.E.; Huynh, Q.K.
Biochem. Biophys. Res. Commun. 187, 480-487, 1992
A;Title: Isolation and characterization of a 25 kDa antifungal protein from flax seeds.
A;Reference number: PC1121; MUID:92392370; PMID:1520338
A;Accession: PC1121
A;Molecule type: protein
A;Residues: 1-37 <BOR>
A;Cross-references: UNIPROT:Q9S8X1
A;Experimental source: seed
C;Superfamily: thaumatin I
C;Keywords: antifungal

Query Match 36.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 15 AASV 18

RESULT 15

AH2787
hypothetical protein Atul718 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2787
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-37 <KUR>
A;Cross-references: UNIPROT:Q8UEN7; GB:AB008688; PIDN:AAL42718.1; PID:gl7740156; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul718
A;Map position: circular chromosome

Query Match 36.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAND 4
Db 10 AAND 13

Search completed: May 5, 2005, 18:25:31
Job time : 21.3333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:01:24 ; Search time 92.3333 Seconds
(without alignments)
61.006 Million cell updates/sec

Title: US-10-827-133-10

Perfect score: 11

Sequence: 1 AANDENYAASV 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	26	Q9UC79	Q9uc79 homo sapien
2	7	63.6	10	P96306	P96306 aeromonas s
3	7	63.6	10	P96321	P96321 escherichia
4	7	63.6	10	P96352	P96352 marinobacte
5	7	63.6	10	Q93LE5	Q93LE5 photobacter
6	5	45.5	14	P96350	P96350 legionella
7	5	45.5	40	Q925P9	Q925P9 cricetus
8	4	36.4	10	P96421	P96421 neisseria g
9	4	36.4	13	Q718T2	Q718T2 newcastle d
10	4	36.4	15	Q9UWH5	Q9UWH5 thermococu
11	4	36.4	15	Q8W4X5	Q8W4X5 arabidopsis
12	4	36.4	18	SODM_MYCHA	P80582 mycobacteri
13	4	36.4	19	Q99MN2	Q99mn2 rattus norv
14	4	36.4	19	Q71ZJ0	Q71zj0 gallus gall
15	4	36.4	20	Q9UWH5	Q9uwh5 vibrio algi
16	4	36.4	20	Q8MI32	Q8mi32 sus scrofa
17	4	36.4	20	Q6LDI5	Q6ldi5 bacillus am
18	4	36.4	20	Q9R4D9	Q9r4d9 escherichia
19	4	36.4	22	Q9UWH5	Q9uwh5 pyrococcus
20	4	36.4	22	Q9S908	Q9s908 sorghum bic
21	4	36.4	22	O85513	O85513 chlamydia t
22	4	36.4	22	O85515	O85515 chlamydia t
23	4	36.4	22	Q9R4W9	Q9r4w9 burkholderi
24	4	36.4	23	Q53469	Q53469 mycobacteri
25	4	36.4	27	Q7RQ41	Q7rq41 plasmodium
26	4	36.4	27	Q9GPK7	Q9gpk7 scutigerell
27	4	36.4	27	Q9S909	Q9s909 zea mays (m
28	4	36.4	27	Q6E269	Q6e269 cucumber mo
29	4	36.4	27	Q9QHC3	Q9qhc3 hepatitis c
30	4	36.4	27	Q9QHC6	Q9qhc6 hepatitis c
31	4	36.4	27	Q9QHC7	Q9qhc7 hepatitis c

32 4 36.4 27 2 Q9QHD1 Q9qhd1 hepatitis c
33 4 36.4 27 2 Q9QHD7 Q9qhd7 hepatitis c
34 4 36.4 27 2 Q9QHD8 Q9qhd8 hepatitis c
35 4 36.4 28 2 Q695M0 Q695m0 brugia mala
36 4 36.4 28 2 Q9K1L8 Q9k1l8 neisseria m
37 4 36.4 29 2 Q9RCT6 Q9rct6 streptococc
38 4 36.4 30 2 Q45356 Q45356 bacillus pu
39 4 36.4 30 2 Q9R5C4 Q9r5c4 comamonas.
40 4 36.4 31 2 Q6X9Z4 Q6x9z4 equus cabal
41 4 36.4 31 2 Q9RCT5 Q9rct5 streptococc
42 4 36.4 31 2 Q83B68 Q83b68 coxiella bu
43 4 36.4 32 1 HCVC_CHEDE P83172 cherax deest
44 4 36.4 32 2 Q9GJS1 Q9gjs1 lagenorhync
45 4 36.4 32 2 Q9GJS2 Q9gjs2 lagenorhync

ALIGNMENTS

RESULT 1
Q9UC79 PRELIMINARY; PRT; 26 AA.
AC Q9UC79; DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin-2 high-molecular-weight form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95217316; PubMed=7702741;
RA Ahmad Z., Ciolek D., Pan Y.C., Michel H., Khan F.R.;
RT "Purification and characterization of a high-molecular-weight form of
recombinant human interleukin-2.";
RL J. Protein Chem. 13:591-598(1994).
DR HSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; F:immune response; IEA.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
SQ SEQUENCE 26 AA; 2887 MW; 5B76889229356ED CRC64;
Query Match 72.7%; Score 8; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AANDENYA 8
Db 16 AANDENYA 23
RESULT 2
P96306 PRELIMINARY; PRT; 10 AA.
AC P96306; DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33658;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";

```

RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 3
P96321 ID P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Kome Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
DR EMBL; U68074; AAB48024.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 4
P96352 ID P96352 PRELIMINARY; PRT; 10 AA.
AC P96352;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonoclasticus (pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OX NCBI_TaxID=2743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49840;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RL RNA 2:1306-1310(1996).

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DR EMBL; U68077; AAB48027.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 5
Q93LE5 ID Q93LE5 PRELIMINARY; PRT; 10 AA.
AC Q93LE5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040837; AAK83525.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 6
P96350 ID P96350 PRELIMINARY; PRT; 14 AA.
AC P96350;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1349 MW; CESF7318D3BE7D7D CRC64;

Query Match
Best Local Similarity 45.5%; Score 5; DB 2; Length 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ANDEN 6
Db 1 ANDEN 5

RESULT 7.
Q925P9
ID Q925P9 PRELIMINARY; PRT; 40 AA.
AC Q925P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Adenosine kinase (EC 2.7.1.20) (Fragment).
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21134654; PubMed=11242543;
RA Singh B., Lin A., Wu Z.C., Gupta R.S.;
RT "Gene structure for adenosine kinase in Chinese hamster and human:
RT high-frequency mutants of CHO cells involve deletions of several
RT introns and exons."
RL DNA Cell Biol. 20:53-65(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97075030; PubMed=8917457;
RA Singh B., Hao W., Wu Z., Bigl B., Gupta R.S.;
RT "Cloning and characterization of cDNA for adenosine kinase from
RT mammalian (Chinese hamster, mouse, human and rat) species. High
RT frequency mutants of Chinese hamster ovary cells involve structural
RT alterations in the gene."
RL Eur. J. Biochem. 241:564-571(1996).
DR EMBL; AF284092; AAK5961.1;
DR HSSP; P55263; 1BX4.
DR GO; GO:0004001; F:adenosine kinase activity; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
KW Kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 40 AA; 4580 MW; CE865B246E807036 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
Db 20 YAASV 24

RESULT 8
P96421
ID P96421 PRELIMINARY; PRT; 10 AA.
AC P96421;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OC NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19424;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
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RL RNA 2:1306-1310(1996).
DR EMBL; U68080; AAB48028.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41AB1A CRC64;

Query Match 36.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDE 5
Db 1 ANDE 4

RESULT 9
Q718T2
ID Q718T2 PRELIMINARY; PRT; 13 AA.
AC Q718T2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemagglutinin-neuraminidase (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Avulavirus.
OC NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RA Gould A.R., Hanson E., Selleck K., Kattenbelt J.A., Mackenzie M.,
RA Della-Porta A.J.;
RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT motifs as markers for viral lineage."
RT Avian Pathol. 32:361-373(2003).
DR EMBL; AF542841; AAI1566.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1628 MW; 685A3336009B645BB CRC64;

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAS 10
Db 8 YAAS 11

RESULT 10
Q9UWH6
ID Q9UWH6 PRELIMINARY; PRT; 15 AA.
AC Q9UWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha
DE (Fragment).
OS Thermococcus litoralis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OC NCBI_TaxID=2265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
RT new and reversible coenzyme A-dependent enzyme involved in peptide
RT fermentation by hyperthermophilic archaea."
RT J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NYAA 9
Db 8 NYAA 11

RESULT 11
Q8W4X5 Q8W4X5 PRELIMINARY; PRT; 15 AA.
AC Q8W4X5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Chl3/nitrate reductase structural protein (Fragment).
GN Name=NIA2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005711; PubMed=1840922;
RA Wilkinson J.Q., Crawford N.M.;
RT "Identification of the Arabidopsis CHL3 gene as the nitrate reductase
structural gene NIA2."
RL Plant Cell 3:461-471(1991).
DR EMBL; S45384; AAL32272.1; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1721 MW; 71C901FC829E1CFD CRC64;

Query Match 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
Db 2 AASV 5

RESULT 12
SODM_MYCHA SODM_MYCHA STANDARD; PRT; 18 AA.
AC P80582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1) (Fragment).
GN Name=sodA; Synonyms=sod;
OS Mycobacterium habana.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1784;
RN [1]
RP SEQUENCE.
RC STRAIN=TW5 5135;
RX MEDLINE=96262709; PubMed=8704977;
RA Bisht D., Mehrotra J., Dhandea M.S., Singh N.B., Sinha S.;
RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the
RT vaccine candidate Mycobacterium habana is superoxide dismutase.";
RL Microbiology 142:1375-1383(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (Probable).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; Sod_Fe_N; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Direct protein sequencing; Manganese; Metal-binding; Oxidoreductase.
FT NON_TER 18
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SQ SEQUENCE 18 AA; 1883 MW; A4161A3DAC93F710 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAS 10
Db 12 YAAS 15

RESULT 13
Q99MN2 Q99MN2 PRELIMINARY; PRT; 19 AA.
AC Q99MN2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Phosphodiesterase 1C (Fragment).
GN Name=PDE1C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RA Prime G.R., Sutor B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF328800; AAK32139.1; -.
FT NON TER 1
SQ SEQUENCE 19 AA; 2129 MW; 1DC5C6D4D5628047 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDEN 6
Db 11 NDEN 14

RESULT 14
Q7LZJO Q7LZJO PRELIMINARY; PRT; 19 AA.
AC Q7LZJO;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Cytochrome P450 PB-B (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RA Gupta R.P., Lapadula D.M., Abou-Donia M.B.;
RT "Purification and characterization of cytochrome P-450 isozymes from
RT phenobarbital-induced adult hen liver.";
RL Comp. Biochem. Physiol. 96:163-176(1990).
DR PIR; B61056; B61056.19
FT NON_TER 19
SQ SEQUENCE 19 AA; 1952 MW; 60CAC347D84E002 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AASV 11
Db 6 AASV 9
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RESULT 15
OMPW_VIBAL
ID OMPW_VIBAL STANDARD; PRT; 20 AA.
AC P83151;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)
DE (Fragment).
GN Name=ompW;
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
alginolyticus and the stability against proteases.",
RL Microbes Environ. 0:0-0(2002).
CC -|- SUBCELLULAR LOCATION: Outer membrane.
CC -|- SIMILARITY: Belongs to the ompW/alkL family.
KW Direct protein sequencing; Outer membrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2096 MW; D29EE7FCA16C0D37 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 AASV 11
Db 12 AASV 15

Search completed: May 5, 2005, 18:22:52
Job time : 94.3333 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:09:44 ; Search time 28 Seconds
(without alignments)
29.326 Million cell updates/sec

Title: US-10-827-133-8
Perfect score: 11
Sequence: 1 AANDENYA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	72.7	11	3	US-09-056-105-33
2	8	72.7	11	3	US-09-425-585-1
3	8	72.7	11	4	US-09-953-321-1
4	8	72.7	11	4	US-08-756-416-1
5	5	45.5	29	4	US-09-270-767-36486
6	5	45.5	29	4	US-09-270-767-51703
7	5	45.5	30	2	US-08-244-657-1
8	5	45.5	31	3	US-09-227-357-398
9	5	45.5	41	4	US-09-493-795B-316
10	4	36.4	4	1	US-08-777-208-1
11	4	36.4	5	3	US-09-125-517A-46
12	4	36.4	5	3	US-09-284-625-10
13	4	36.4	5	4	US-08-877-605-324
14	4	36.4	5	6	5217869-73
15	4	36.4	5	6	5217869-73
16	4	36.4	6	3	US-09-125-517A-5
17	4	36.4	6	3	US-08-485-355B-25
18	4	36.4	6	4	US-08-877-605-315
19	4	36.4	6	4	US-08-877-605-334
20	4	36.4	7	4	US-08-877-605-342
21	4	36.4	8	3	US-08-688-988-48
22	4	36.4	8	6	5436138-14
23	4	36.4	8	6	5436138-14
24	4	36.4	9	1	US-08-480-547A-2
25	4	36.4	9	1	US-08-250-847B-2
26	4	36.4	9	2	US-08-408-095-4
27	4	36.4	9	2	US-08-463-949A-2

28 4 36.4 9 3 US-08-396-385-12 Sequence 12, Appl
29 4 36.4 9 3 US-08-464-410A-2 Sequence 2, Appl
30 4 36.4 9 3 US-08-159-339A-142 Sequence 142, Appl
31 4 36.4 9 3 US-08-159-339A-162 Sequence 162, Appl
32 4 36.4 9 3 US-08-159-339A-178 Sequence 178, Appl
33 4 36.4 9 3 US-08-159-339A-197 Sequence 197, Appl
34 4 36.4 9 3 US-08-772-282-29 Sequence 29, Appl
35 4 36.4 9 3 US-09-287-221-12 Sequence 12, Appl
36 4 36.4 9 4 US-09-543-608A-50 Sequence 50, Appl
37 4 36.4 9 4 US-09-239-043D-2494 Sequence 2494, Appl
38 4 36.4 9 5 PCT-US94-06066-2 Sequence 2, Appl
39 4 36.4 9 5 PCT-US96-00888-5 Sequence 5, Appl
40 4 36.4 10 2 US-08-518-967-8 Sequence 8, Appl
41 4 36.4 10 3 US-08-159-339A-148 Sequence 148, Appl
42 4 36.4 11 1 US-07-723-002C-14 Sequence 14, Appl
43 4 36.4 11 3 US-09-208-966-8 Sequence 8, Appl
44 4 36.4 11 3 US-09-208-966-53 Sequence 53, Appl
45 4 36.4 11 4 US-09-268-480-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-056-105-33
; Sequence 33, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: E.Coli
US-09-056-105-33

Query Match 72.7%; Score 8; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.025; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0

OY 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 2
US-09-425-585-1
; Sequence 1, Application US/09425585
; Patent No. 634815
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOSEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT

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; ORGANISM: Escherichia coli
US-09-425-585-1

Query Match      72.7%; Score 8; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AANDENYA 8
Db      1 AANDENYA 8
|||||||

RESULT 3
US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match      72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AANDENYA 8
Db      1 AANDENYA 8
|||||||

RESULT 4
US-08-756-416-1
; Sequence 1, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Fell, Perry
; APPLICANT: Mittler, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
; TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755
; FILING DATE: 30-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.41US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-756-416-1

Query Match      72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AANDENYA 8
Db      1 AANDENYA 8
|||||||

RESULT 5
US-09-270-767-36486
; Sequence 36486, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36486
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-36486

Query Match      45.5%; Score 5; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 68;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 NYAAA 10
Db      10 NYAAA 14
|||||||

RESULT 6
US-09-270-767-51703
; Sequence 51703, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51703
; LENGTH: 29
; TYPE: PRT
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ORGANISM: Drosophila melanogaster
US-09-270-767-51703

Query Match 45.5%; Score 5; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 10 NYAAA 14

RESULT 7

US-08-244-657-1
Sequence 1, Application US/08244657
Patent No. 5902736
GENERAL INFORMATION:
APPLICANT: YAMADA, Hideaki
APPLICANT: SHIMIZU, Sakayu
APPLICANT: IKENAKA, Yasuhiro
APPLICANT: YAJIMA, Kazuyoshi
APPLICANT: YAMADA, Yukio
APPLICANT: NAMBA, Hirokazu
APPLICANT: TAKANO, Masayuki
APPLICANT: TAKAHASHI, Satomi
TITLE OF INVENTION: Process For The Production of D-a-Amino
Acids
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,657
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/JP93/01408
FILING DATE: 01-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 265914/1992
FILING DATE: 05-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 74129/185/AOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-244-657-1
Qy 6 NYAAA 10
Db 5 NYAAA 9

Query Match 45.5%; Score 5; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 5 NYAAA 9

RESULT 8
US-09-227-357-398
Sequence 398, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT FILING DATE: 1999-01-08
CURRENT APPLICATION NUMBER: US/09/227,357
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660

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; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 398
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-398

Query Match          45.5%; Score 5; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 14 NYAAA 18

RESULT 9
US-09-493-795B-316
; Sequence 316, Application US/09493795B
; Patent No. 6797808
; GENERAL INFORMATION:
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Alpha-Conotoxin Peptides
; FILE REFERENCE: 2314-179-A
; CURRENT APPLICATION NUMBER: US/09/493,795B
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/118,381
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 404
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 316
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus catus
US-09-493-795B-316

Query Match          45.5%; Score 5; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDE 5
Db 7 AANDE 11

RESULT 10
US-08-777-208-1
; Sequence 1, Application US/08777208
; Patent No. 5763576
; GENERAL INFORMATION:
; APPLICANT: Powers, James C.
; TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Deveau, Colton & Marquis
; STREET: Two Midtown Plaza, Suite 1400
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Dikette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,208
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/539944
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colton, Laurence P.
; REGISTRATION NUMBER: 33371
; REFERENCE/DOCKET NUMBER: 10733-191B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 875-3555
; TELEFAX: (404) 875-8505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; US-08-777-208-1

Query Match          36.4%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ARAV 11
Db 1 ARAV 4

RESULT 11
US-09-125-517A-46
; Sequence 46, Application US/09125517A
; Patent No. 6087336
; GENERAL INFORMATION:
; APPLICANT: Cotton, Ronald
; APPLICANT: Edwards, Philip Neil
; APPLICANT: Luke, Richard William Arthur
; TITLE OF INVENTION: Peptide Derivatives
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth St., N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,517A
; FILING DATE: 20-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9603855.9
; FILING DATE: 23-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9620819.4
; FILING DATE: 05-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1991-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 46:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-125-517A-46

Query Match 36.4%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
Db 2 AAAY 5

RESULT 12
US-09-284-625-10
; Sequence 10, Application US/09284625
; Patent No. 6207644
; GENERAL INFORMATION:
; APPLICANT: Luke, Richard William
; TITLE OF INVENTION: Peptide Analogues Containing a 7-membered Lactam Ring
; FILE REFERENCE: 1991-169
; CURRENT APPLICATION NUMBER: US/09/284,625
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/GB97/02837
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: GB 96218367
; PRIOR FILING DATE: 1996-10-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-625-10

Query Match 36.4%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
Db 2 AAAY 5

RESULT 13
US-08-877-605-324
; Sequence 324, Application US/08877605
; Patent No. 6562965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Z Library
US-08-877-605-324

Query Match 36.4%; Score 4; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
Db 1 AAAY 4

RESULT 14
5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73:
; LENGTH: 5
5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
Db 2 AAND 5

RESULT 15
5217869-73
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:73:
; LENGTH: 5
5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
Db 2 AAND 5

Search completed: May 5, 2005, 18:24:17
Job time : 29 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:18:20 ; Search time 78 Seconds
(without alignments)
47.046 Million cell updates/sec

Title: US-10-827-133-8

Perfect score: 11

Sequence: 1 AANDENYAAAV 11

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Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	72.7	11	US-09-953-321-1	Sequence 1, Appli
2	8	72.7	11	US-09-975-132A-3	Sequence 3, Appli
3	8	72.7	11	US-10-289-135A-119	Sequence 119, App
4	8	72.7	12	US-10-080-866-19	Sequence 19, Appl
5	6	54.5	16	US-10-037-243-3	Sequence 3, Appli
6	5	45.5	31	US-09-983-802-398	Sequence 398, App
7	5	45.5	31	US-09-984-490-398	Sequence 398, App
8	5	45.5	31	US-09-973-278-508	Sequence 508, App
9	5	45.5	41	US-10-895-372-316	Sequence 316, App
10	4	36.4	4	US-09-837-537B-1	Sequence 1, Appli
11	4	36.4	4	US-10-427-208-17	Sequence 17, Appl
12	4	36.4	6	US-09-991-262-25	Sequence 25, Appl
13	4	36.4	8	US-10-007-761-30	Sequence 30, Appl

14	4	36.4	8	15	US-10-435-608-27	Sequence 27, Appl
15	4	36.4	8	15	US-10-622-108-27	Sequence 27, Appl
16	4	36.4	8	17	US-10-842-054-6	Sequence 6, Appli
17	4	36.4	8	17	US-10-841-250-31	Sequence 31, Appl
18	4	36.4	8	17	US-10-841-250-81	Sequence 81, Appl
19	4	36.4	8	17	US-10-841-250-94	Sequence 94, Appl
20	4	36.4	8	17	US-10-841-250-102	Sequence 102, Appl
21	4	36.4	9	8	US-08-452-843A-1	Sequence 1, Appli
22	4	36.4	9	8	US-08-344-824-17	Sequence 17, Appl
23	4	36.4	9	9	US-09-988-019-29	Sequence 29, Appl
24	4	36.4	9	10	US-09-809-638-119	Sequence 119, App
25	4	36.4	9	11	US-09-935-476-8	Sequence 8, Appli
26	4	36.4	9	14	US-10-115-515-2	Sequence 2, Appli
27	4	36.4	9	14	US-10-057-789-246	Sequence 246, App
28	4	36.4	9	14	US-10-212-628-246	Sequence 246, App
29	4	36.4	9	15	US-10-149-138-4203	Sequence 4203, Ap
30	4	36.4	9	15	US-10-149-138-4204	Sequence 4204, Ap
31	4	36.4	9	15	US-10-149-138-4205	Sequence 4205, Ap
32	4	36.4	9	15	US-10-149-138-4206	Sequence 4206, Ap
33	4	36.4	9	15	US-10-149-138-4365	Sequence 4365, Ap
34	4	36.4	9	15	US-10-149-138-4366	Sequence 4366, Ap
35	4	36.4	9	15	US-10-149-138-4367	Sequence 4367, Ap
36	4	36.4	9	15	US-10-149-138-4369	Sequence 4369, Ap
37	4	36.4	9	15	US-10-149-138-4370	Sequence 4370, Ap
38	4	36.4	9	15	US-10-149-138-4371	Sequence 4371, Ap
39	4	36.4	9	15	US-10-149-135-2190	Sequence 2190, Ap
40	4	36.4	9	15	US-10-149-135-2191	Sequence 2191, Ap
41	4	36.4	9	15	US-10-149-135-2192	Sequence 2192, Ap
42	4	36.4	9	15	US-10-149-135-2193	Sequence 2193, Ap
43	4	36.4	9	15	US-10-149-135-2305	Sequence 2305, Ap
44	4	36.4	9	15	US-10-149-135-2306	Sequence 2306, Ap
45	4	36.4	9	15	US-10-149-135-2307	Sequence 2307, Ap

ALIGNMENTS

RESULT 1

US-09-953-321-1
; Sequence 1, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953.321
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-953-321-1

Query Match 72.7%; Score 8; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDENYA 8

Db 1 AANDENYA 8

RESULT 2

US-09-975-132A-3
; Sequence 3, Application US/09975132A
; Publication No. US20020182672A1

; GENERAL INFORMATION:
; APPLICANT: Kolkman, Marc
; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a
; TITLE OF INVENTION: Microorganism
; FILE REFERENCE: GC636-2
; CURRENT APPLICATION NUMBER: US/09/975,132A
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/239,531
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide tag
US-09-975-132A-3

Query Match 72.7%; Score 8; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 3
US-10-289-135A-119
; Sequence 119, Application US/10289135A
; Publication No. US20030180937A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIU, GEORGE
; APPLICANT: DELISA, MATTHEW
; TITLE OF INVENTION: ENGINEERING OF LEADER PEPTIDES FOR THE SECRETION OF
; TITLE OF INVENTION: RECOMBINANT PROTEINS IN BACTERIA
; FILE REFERENCE: CLFR.019US
; CURRENT APPLICATION NUMBER: US/10/289,135A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/337,452
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-289-135A-119

Query Match 72.7%; Score 8; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 4
US-10-080-866-19
; Sequence 19, Application US/10080866
; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Paegle, E. Sasha
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1732R1
; CURRENT APPLICATION NUMBER: US/10/080,866

; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/274,384
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide for generating antibodies
US-10-080-866-19

Query Match 72.7%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 2 AANDENYA 9

RESULT 5
US-10-037-243-3
; Sequence 3, Application US/10037243
; Publication No. US20030134352A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, LLC.
; APPLICANT: Freimuth, Paul I
; APPLICANT: Zhang, Yian-Biao
; APPLICANT: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
; FILE REFERENCE: BSA 01-22
; CURRENT APPLICATION NUMBER: US/10/037,243
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
US-10-037-243-3

Query Match 54.5%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDEN 6
Db 1 AANDEN 6

RESULT 6
US-09-983-802-398
; Sequence 398, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

[illegible]

RESULT 7

US-09-984-490-398

Sequence 398, Application US/09984490

Publication No. US2003064412A1

GENERAL INFORMATION:

APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins

FILE REFERENCE: P2010P1

CURRENT APPLICATION NUMBER: US/09/984,490

CURRENT FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684

PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 398
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-984-490-398

Query Match 45.5%; Score 5; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10
 Db 14 NYAAA 18

RESULT 8

US-09-973-278-508
 ; Sequence 508, Application US/09973278
 ; Publication No. US20040044191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer et al.
 ; TITLE OF INVENTION: 123 Human Secreted Proteins
 ; FILE REFERENCE: P2010P2
 ; CURRENT APPLICATION NUMBER: US/09/973,278
 ; CURRENT FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: 60/239,899
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 09/227,357
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/13684
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/051,926
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/052,793
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,925
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,929
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/052,803
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/052,732
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,931
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,932
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,916
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,930
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,918
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,920
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/052,733
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/052,795
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,919
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,928
 ; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/055,722

; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,723
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,948
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,949
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,953
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,950
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,947
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,964
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/056,360
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,684
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,984
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/055,954
 ; PRIOR FILING DATE: 1997-08-18
 ; PRIOR APPLICATION NUMBER: 60/058,785
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,664
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,660
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,661
 ; PRIOR FILING DATE: 1997-09-12
 ; NUMBER OF SEQ ID NOS: 947
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 508
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-973-278-508

Query Match 45.5%; Score 5; DB 11; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10
 Db 14 NYAAA 18

RESULT 9

US-10-895-372-316
 ; Sequence 316, Application US/10895372
 ; Publication No. US20050032705A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Hillyard, David R.
 ; APPLICANT: McIntosh, J. Michael
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: Alpha-Conotoxin Peptides
 ; FILE REFERENCE: 2314-286
 ; CURRENT APPLICATION NUMBER: US/10/895,372
 ; CURRENT FILING DATE: 2004-07-21
 ; PRIOR APPLICATION NUMBER: US 09/493,795
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/118,381
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 404
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 316
 ; LENGTH: 41
 ; TYPE: PRT
 ; ORGANISM: Conus catus
 US-10-895-372-316

Query Match 45.5%; Score 5; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANDE 5
DB 7 AANDE 11

RESULT 10
US-09-837-537B-1
; Sequence 1, Application US/09837537B
; Publication No. US20020061839A1
; GENERAL INFORMATION:
; APPLICANT: SCHARPE, Simon Lodewijk
; APPLICANT: DE MEESTER, Ingrid Anna Jozef
; APPLICANT: BELIAEV, Alexandre Arkadievitch
; APPLICANT: LAMBEIR, Anne-Marie Virginie Renee
; APPLICANT: AUGUSTYNS, Koen Jan Ludovicus
; APPLICANT: HAEMERS, Achiel Jean-Marie
; APPLICANT: GOOSSENS, Filip Jozef Anny
; APPLICANT: HENDRIKS, Dirk Frans
; TITLE OF INVENTION: Serine Peptidase Modulators
; FILE REFERENCE: 702 010673
; CURRENT APPLICATION NUMBER: US/09/837,537B
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: EP 98200733.8
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: MS Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Functional group linked by Suc and MeO to phosphorus atom
; OTHER INFORMATION: in serine peptidase/protease modulating compound
US-09-837-537B-1

Query Match 36.4%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAV 11
DB 1 AAAV 4

RESULT 11
US-10-427-208-17
; Sequence 17, Application US/10427208
; Publication No. US20030200555A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hazuda, Daria J
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Lai, Ming-Tain
; APPLICANT: Xu, Min
; APPLICANT: Shi, Xiao-Ping
; APPLICANT: Simon, Adam J.
; APPLICANT: Wu, Guoxin
; APPLICANT: Li, Yueying
; APPLICANT: Register, Robert B.
; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED
; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 21052
; CURRENT APPLICATION NUMBER: US/10/427,208
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 4

; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: novel sequence of known enzyme cleavage site
US-10-427-208-17

Query Match 36.4%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAA 9
DB 1 NYAA 4

RESULT 12
US-09-991-262-25
; Sequence 25, Application US/09991262
; Publication No. US20030041349A1
; GENERAL INFORMATION:
; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
; TITLE OF INVENTION: Insect Viruses and Their Uses in
; Protecting Plants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/991,262
; FILING DATE: 20-NO. US20030041349A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,238
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: US 08/485,355
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/440,522
; FILING DATE: 12-MAY-1995
; APPLICATION NUMBER: US 08/089,372
; FILING DATE: 08-JUL-1993
; APPLICATION NUMBER: AU PL4081/92
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-991-262-25

Query Match 36.4%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|||||
Db 2 AAAY 5

RESULT 13

US-10-007-761-30
; Sequence 30, Application US/10007761
; Publication No. US20020150984A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Peptides for Activation and Inhibition
; FILE REFERENCE: 58600-8208.US00
; CURRENT APPLICATION NUMBER: US/10/007,761
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/262,060
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-delta RACK peptide
US-10-007-761-30

Query Match 36.4%; Score 4; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAND 4
|||||
Db 3 AAND 6

RESULT 14

US-10-435-608-27
; Sequence 27, Application US/10435608
; Publication No. US2003023536A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Lencer, Wayne I.
; APPLICANT: Simister, Neil E.
; APPLICANT: Bitonti, Alan J.
; TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTIC
; FILE REFERENCE: S01383.70010.US
; CURRENT APPLICATION NUMBER: US/10/435,608
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: PCT/US02/21335
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-435-608-27

Query Match 36.4%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|||||
Db 5 AAAY 8

RESULT 15

US-10-622-108-27

; Sequence 27, Application US/10622108
; Publication No. US20040063912A1
; GENERAL INFORMATION:
; APPLICANT: Blumberg, Richard S.
; APPLICANT: Lencer, Wayne I.
; APPLICANT: Simister, Neil E.
; APPLICANT: Bitonti, Alan J.
; TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTIC
; FILE REFERENCE: S01383.70011.US
; CURRENT APPLICATION NUMBER: US/10/622,108
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 10/435,608
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: PCT/US02/21355
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/364,482
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide
US-10-622-108-27

Query Match 36.4%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|||||
Db 5 AAAY 8

Search completed: May 5, 2005, 18:31:03
Job time : 79 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:01:24 ; Search time 92.3333 Seconds
(without alignments)
61.006 Million cell updates/sec

Title: US-10-827-133-8
Perfect score: 11
Sequence: 1 AANDENYAAV 11

Scoring table: OLIGO
Gapop 60.0 ; Gapext 60.0
Searched: 1612378 seqs, 512079187 residues
Word size : 0

Total number of hits satisfying chosen parameters: 68540

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	26	2 Q9UC79	Q9UC79 homo sapien
2	7	63.6	10	2 P96306	P96306 aeromonas s
3	7	63.6	10	2 P96321	P96321 escherichia
4	7	63.6	10	2 P96352	P96352 marinobacte
5	7	63.6	10	2 Q93LES	Q93LES photobacter
6	5	45.5	14	2 P96350	P96350 legionella
7	5	45.5	15	2 Q9UWH6	Q9UWH6 thermococcu
8	5	45.5	22	2 Q9UWH5	Q9UWH5 pyrococcus
9	5	45.5	30	2 Q9R5C4	Q9R5C4 comamonas
10	4	36.4	8	2 Q7M3L7	Q7M3L7 ascidia cer
11	4	36.4	10	2 P96421	P96421 neisseria g
12	4	36.4	12	2 Q6EEI9	Q6EEI9 sus scrofa
13	4	36.4	12	2 Q9EQV3	Q9EQV3 mus musculu
14	4	36.4	15	2 Q47893	Q47893 fremyella d
15	4	36.4	17	2 Q79AV8	Q79AV8 escherichia
16	4	36.4	18	2 Q64353	Q64353 bacterioph
17	4	36.4	19	2 Q9UR67	Q9UR67 aspergillus
18	4	36.4	19	2 Q99MN2	Q99MN2 rattus norv
19	4	36.4	19	2 Q96396	Q96396 suid herpes
20	4	36.4	20	1 TLP ACTCH	P83958 actinidia c
21	4	36.4	20	2 Q29341	Q29341 sus scrofa
22	4	36.4	20	2 Q9R4D9	Q9R4D9 escherichia
23	4	36.4	20	2 Q9AW46	Q9AW46 brachydanio
24	4	36.4	22	2 Q9N6J2	Q9N6J2 balanus amp
25	4	36.4	22	2 Q9NDS9	Q9NDS9 balanus amp
26	4	36.4	22	2 Q9NDT8	Q9NDT8 balanus amp
27	4	36.4	22	2 Q85513	Q85513 chlamydia t
28	4	36.4	22	2 Q85515	Q85515 chlamydia t
29	4	36.4	22	2 Q9R4W9	Q9R4W9 burkholderi
30	4	36.4	22	2 Q87084	Q87084 suid herpes
31	4	36.4	22	2 Q87085	Q87085 suid herpes

32	4	36.4	23	2 Q76N57	Q76N57 homo sapien
33	4	36.4	23	2 Q68983	Q68983 suid herpes
34	4	36.4	23	2 Q69391	Q69391 suid herpes
35	4	36.4	23	2 Q69392	Q69392 suid herpes
36	4	36.4	23	2 Q69393	Q69393 suid herpes
37	4	36.4	23	2 Q69395	Q69395 suid herpes
38	4	36.4	23	2 Q87078	Q87078 suid herpes
39	4	36.4	23	2 Q87079	Q87079 suid herpes
40	4	36.4	23	2 Q87080	Q87080 suid herpes
41	4	36.4	23	2 Q87081	Q87081 suid herpes
42	4	36.4	23	2 Q87082	Q87082 suid herpes
43	4	36.4	23	2 Q87083	Q87083 suid herpes
44	4	36.4	23	2 Q87086	Q87086 suid herpes
45	4	36.4	24	1 ATPE_MICLU	P80286 micrococcus

ALIGNMENTS

RESULT 1
Q9UC79 PRELIMINARY; PRT; 26 AA.
AC Q9UC79; DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Interleukin-2 high-molecular-weight form (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95217136; PubMed=7702741;
RA Ahmad Z., Ciolek D., Pan Y.C., Michel H., Khan F.R.;
RT "Purification and characterization of a high-molecular-weight form of recombinant human interleukin-2";
RL J. Protein Chem. 13:591-598(1994)
RL HSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
SQ SEQUENCE 26 AA; 2887 MW; 5B766892229356ED CRC64;
Query Match 72.7%; Score 8; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AANDENYA 8
Db 16 AANDENYA 23
RESULT 2
P96306 PRELIMINARY; PRT; 10 AA.
ID P96306
AC P96306;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33658;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";

```

RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYA 8
DB 1 ANDENYA 7

RESULT 3
P96321 ID P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=9972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Komine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
DR EMBL; U68074; AAB48024.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYA 8
DB 1 ANDENYA 7

RESULT 4
P96352 ID P96352 PRELIMINARY; PRT; 10 AA.
AC P96352;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OX NCBI_TaxID=2743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49840;
RX MEDLINE=97128184; PubMed=9972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).

```

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DR EMBL; U68077; AAB48027.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 63.6%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYA 8
DB 1 ANDENYA 7

RESULT 5
Q93LE5 ID Q93LE5 PRELIMINARY; PRT; 10 AA.
AC Q93LE5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20083247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tmRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040837; AAK83525.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDENYA 8
DB 1 ANDENYA 7

RESULT 6
P96350 ID P96350 PRELIMINARY; PRT; 14 AA.
AC P96350;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=9972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026.1; -.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1349 MW; CESF7318D3BE7D7D CRC64;

Query Match
Best Local Similarity 45.5%; Score 5; DB 2; Length 14;
Matches 100.0%; Pred. No. 1.8e+02;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDEN 6

Db 1 ANDEN 5

RESULT 7

Q9UWH6 PRELIMINARY; PRT; 15 AA.
AC Q9UWH6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha (Fragment).
DE Thermococcus litoralis.
OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=2265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea.";
RT J. Bacteriol. 178:780-787(1996).
RL J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 15 AA; 1549 MW; 0C1766910B222944 CRC64;

Query Match 45.5%; Score 5; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10

Db 8 NYAAA 12

RESULT 8

Q9UWH5 PRELIMINARY; PRT; 22 AA.
AC Q9UWH5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha (Fragment). furiosus.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea.";
RT J. Bacteriol. 178:780-787(1996).
RL J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 22 AA; 2465 MW; 684CBA3B5D750A0D CRC64;

Query Match 45.5%; Score 5; DB 2; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10

Db 13 NYAAA 17

RESULT 9

Q9R5C4 PRELIMINARY; PRT; 30 AA.

ID Q9R5C4 PRELIMINARY; PRT; 30 AA.

AC Q9R5C4;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

DE N-carbamoyl-D-amino acid amidohydrolase (Fragment).

OS Comamonas.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae.

OX NCBI_TaxID=283;

RN [1]

RP SEQUENCE.

RX MEDLINE=93215645; PubMed=8462543;

RA Ogawa J., Shimizu S., Yamada H.;

RT "N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c purification and characterization.";

RL Eur. J. Biochem. 212:685-691(1993).

SQ SEQUENCE 30 AA; 3323 MW; CBA003DE1A22133F CRC64;

Query Match 45.5%; Score 5; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10

Db 5 NYAAA 9

RESULT 10

Q7M3L7 PRELIMINARY; PRT; 8 AA.

AC Q7M3L7;

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Blood cell protein A8 (Fragment).

OS Ascidia ceratodes.

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

OC Phlebobranchia; Ascidiidae; Ascidia.

OX NCBI_TaxID=30276;

RN [1]

RP SEQUENCE.

RX MEDLINE=96132650; PubMed=8554314; DOI=10.1006/abbi.1995.0035;

RA Taylor S.W., Ross M.M., Waite J.H.;

RT "Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing

polypeptides from the blood cells of the ascidians Ascidia ceratodes

and Molgula manhattensis.";

RL Arch. Biochem. Biophys. 324:228-240(1995).

DR PIR; S68325; S68325.

FT NON_TER 1 1

FT NON_TER 8 8

SQ SEQUENCE 8 AA; 907 MW; D9DDDDDCB4B4B5A CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAA 10

Db 4 YAAA 7

RESULT 11

P96421 PRELIMINARY; PRT; 10 AA.

AC P96421;

DT 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE Coded portion of proteolysis tag (Fragment).

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

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OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19424;
RA MEDLINE=97128184; PubMed=8972778;
RX Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68080; AAB48028.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41AB1A CRC64;

Query Match 36.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDE 5
Db 1 ANDE 4

RESULT 12
Q6EEI9 PRELIMINARY; PRT; 12 AA.
AC Q6EEI9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE CAMKI-like protein kinase (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonnenan D., Rohrer G.A.;
RT "Comparative mapping of human chromosome 10 to pig chromosomes 10 and
RT 14.";
RL Anim. Genet. 35:338-343 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Nonnenan D.J., Rohrer G.A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY368181; AAR24386.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1259 MW; CF317FF387CDDDD CRC64;

Query Match 36.4%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAVV 11
Db 5 AAVV 8

RESULT 13
Q9EQV3 PRELIMINARY; PRT; 12 AA.
AC Q9EQV3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-sarcoglycan (Fragment).
GN Name=Sgca;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21099368; PubMed=11179961;
RA Wakabayashi-Takai E., Noguchi S., Ozawa E.;
RT "Identification of mouse genesis-dependent transcriptional enhancers in
RT promoter region of mouse gamma-sarcoglycan gene.";
RL Eur. J. Biochem. 268:948-957(2001).
DR EMBL; AB044625; BAB18770.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1257 MW; D382726D594361B2 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAVV 11
Db 2 AAVV 5

RESULT 14
Q47893 PRELIMINARY; PRT; 15 AA.
AC Q47893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Beta-phycocyanin (Fragment).
OS Fremvella diplosiphon (Fragment).
OC Bacteria; Cyanobacteria; Calothrix PCC 7601).
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=3086870;
RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
RT the genome of the cyanobacterium Fremyella diplosiphon.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
DR EMBL; M13217; AAA24880.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1528 MW; 7FF2F65518F493DA CRC64;

Query Match 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAVV 11
Db 11 AAVV 14

RESULT 15
Q79AV8 PRELIMINARY; PRT; 17 AA.
AC Q79AV8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Gene malG for maltose transport (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86081738; PubMed=3000770;
RA Dassa E., Hofnung M.;
RT "Sequence of gene malG in E. coli K12: homologies between integral
RT membrane components from binding protein-dependent transport
RT systems.";
RL EMBO J. 4:2287-2293(1985).
DR EMBL; X02871; CAA26629.1; -.
FT NON_TER 17

```


SQ SEQUENCE 17 AA; 1878 MW; E6C439F48AB27EED CRC64;

Query Match 36.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAA 10

Db 7 YAAA 10

Search completed: May 5, 2005, 18:22:48
Job time : 95.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds
(without alignments)
52.052 Million cell updates/sec

Title: US-10-827-133-8
Perfect score: 11
Sequence: 1 AANDENYAAAV 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	45.5	30	2 S30333	N-carbamoyl-D-amin
2	4	36.4	8	2 S68325	blood cell protein
3	4	36.4	18	2 T13132	protein gp45.1 - p
4	4	36.4	24	2 A24802	cuticle protein 7
5	4	36.4	25	2 A61148	cytidase (EC 3.5.
6	4	36.4	27	2 S05219	photosystem I chai
7	4	36.4	28	2 E81239	hypothetical prote
8	4	36.4	30	2 I39799	CAT-66 - Bacillus
9	4	36.4	30	2 B47607	immunogenic protei
10	4	36.4	32	2 F60529	hemocyanin M1 - cr
11	4	36.4	34	2 PC1319	large granule L9 c
12	4	36.4	34	2 A87279	hypothetical prote
13	4	36.4	36	2 C84175	hypothetical prote
14	4	36.4	37	2 A32000	somatostatin, panc
15	4	36.4	37	2 S17684	thumatin homolog
16	4	36.4	37	2 S4210	hypothetical prote
17	4	36.4	37	2 AH2787	hypothetical prote
18	4	36.4	38	2 S07140	ribosomal protein
19	4	36.4	38	2 H95005	hypothetical prote
20	4	36.4	38	2 G81904	hypothetical prote
21	4	36.4	39	2 AB930	hypothetical prote
22	4	36.4	39	2 AF0836	probable bacteriop
23	4	36.4	41	2 S00776	hypothetical prote
24	4	36.4	41	2 E82544	hypothetical prote
25	4	36.4	42	2 D37416	bloodstream-specif
26	4	36.4	44	1 BXSAL	antibacterial prot
27	4	36.4	45	2 PNO590	tyrosine 3-monooxy
28	4	36.4	45	2 PNO589	tyrosine 3-monooxy
29	4	36.4	45	2 B40432	calpain (EC 3.4.22

30 4 36.4 46 2 B45174 eye cell developme
31 4 36.4 47 2 AB2489 hypothetical prote
32 4 36.4 48 2 AB4368 hypothetical prote
33 4 36.4 49 2 G44530 T-cell receptor al
34 4 36.4 49 2 T35952 hypothetical prote
35 3 27.3 5 2 S5237 zinc-binding prote
36 3 27.3 5 2 PT0281 Ig heavy chain CRD
37 3 27.3 5 2 A32014 trAm protein - Esc
38 3 27.3 5 2 JS0319 subesophageal gang
39 3 27.3 6 2 S66195 alcohol dehydrogen
40 3 27.3 8 2 PQ0726 unidentified 4.5/4
41 3 27.3 8 2 H41978 calliferramide 8 -
42 3 27.3 8 2 A61467 penalbumin - Adeli
43 3 27.3 9 2 PT0272 Ig heavy chain CRD
44 3 27.3 9 2 A43848 cell surface adhes
45 3 27.3 9 2 A60427 macrophage cytotox

ALIGNMENTS

RESULT 1

S30333
N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp. (fragment)
C:Species: Comamonas sp.
C:Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000
C:Accession: S30333
R:Ogawa, J.; Shimizu, S.; Yamada, H.
Eur. J. Biochem. 212, 685-691, 1993
A:Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c. Purification
A:Reference number: S30333; MUID:93215645; PMID:8462543
A:Accession: S30333
A:Molecule type: protein
A:Residues: 1-30 <OGA>
A:Experimental source: strain E222c
C:Function:
A:Description: amidohydrolase with strict specificity for the D-form and strict substrata:
bamoyl-DL-aspartate
C:Superfamily: hypothetical protein YLR351c
C:Keywords: hydrolase

Query Match 45.5%; Score 5; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NYAAA 10
|||
DB 5 NYAAA 9

RESULT 2

S68325
blood cell protein A8 - Ascidia ceratodes (fragment)
N:Alternate names: Abcp-A

C:Species: Ascidia ceratodes
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C:Accession: S68325
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from tr

A:Reference number: S68325; MUID:96132650; PMID:8554314

A:Accession: S68325

A:Molecule type: protein

A:Residues: 1-8 <TAY>

A:Cross-references: UNIPROT:Q7M3L7

F12,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 YAAA 10
|||

Db 4 YAAA 7

RESULT 3
T13132
protein gp45.1 - phage N15
C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13132
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z17603
A;Accession: T13132
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <EN>
A;Cross-references: UNIPROT:O64353; EMBL:AF064539; NID:g3192683; PID:g3192731; PIDN:AACT
C;Genetics:
A;Note: gene 45.1

Query Match 36.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11
|||||
Db 10 AAAV 13

RESULT 4
A24802
cuticle protein 7 - migratory locust (fragment)
C;Species: Locusta migratoria (migratory locust)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
C;Accession: A24802
R;Hojrup, P.; Andersen, S.O.; Roepstorff, P.
Eur J. Biochem. 154, 153-159, 1986
A;Reference number: A91157; MUID:86108304; PMID:3943519
A;Accession: A24802
A;Molecule type: protein
A;Residues: 1-24 <HOJ>
A;Cross-references: UNIPROT:P11733

Query Match 36.4%; Score 4; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAAA 10
|||||
Db 7 YAAA 10

RESULT 5
A61148
cyanidase (EC 3.5.5.-) - Alcaligenes denitrificans (strain DF3) (fragment)
C;Species: Alcaligenes denitrificans
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: A61148
R;Ingvorsen, K.; Hojer-Pedersen, B.; Godtfredsen, S.E.
Appl. Environ. Microbiol. 57, 1783-1789, 1991
A;Title: Novel cyanide-hydrolyzing enzyme from Alcaligenes xylosoxidans subsp. denitrifi
A;Reference number: A61148; MUID:91336720; PMID:1872607
A;Accession: A61148
A;Molecule type: protein
A;Residues: 1-25 <ING>
A;Cross-references: UNIPROT:Q7M0N8
C;Keywords: hydrolase

Query Match 36.4%; Score 4; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11

Db 11 AAAV 14
|||||

RESULT 6
S05219
photosystem I chain III - Synechococcus sp. (fragment)
N;Alternate names: photosystem I L4K protein; photosystem I plastocyanin-binding chain
C;Species: Synechococcus sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Apr-1999
C;Accession: S05219
R;Koike, H.; Ikeuchi, M.; Hiyama, T.; Inoue, Y.
FEBS Lett. 253, 257-263, 1989
A;Title: Identification of photosystem I components from the cyanobacterium, Synechococ
A;Reference number: S05218; MUID:89338747; PMID:2503399
A;Accession: S05219
A;Molecule type: protein
A;Residues: 1-27 <KOI>
A;Note: the authors identified this protein as photosystem I chain IV
R;Koike, H.; Ikeuchi, M.; Hiyama, T.; Inoue, Y.
FEBS Lett. 258, 180B, 1989
A;Reference number: S06842
A;Contents: annotation; erratum
A;Note: this is a revision to the identification of the sequence in reference S05218
C;Genetics:
A;Gene: psaf
C;Superfamily: photosystem I chain III
C;Keywords: photosynthesis; photosystem I; thylakoid

Query Match 36.4%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11
|||||
Db 19 AAAV 22

RESULT 7
E81239
hypothetical protein NMB0093 [imported] - Neisseria meningitidis (strain MC58 serogroup E
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: E81239
R;Rettlein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81239
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <TET>
A;Cross-references: UNIPROT:Q9K1L8; GB:AE002368; GB:AE002098; NID:g7225303; PIDN:AAF4055
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0093

Query Match 36.4%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NDEN 6
|||||
Db 3 NDEN 6

RESULT 8
I39799
CAT-66 - Bacillus pumilus (fragment)
C;Species: Bacillus pumilus

C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I39799
 R:Duval, E.J.; Williams, D.M.; Mongkolsuk, S.; Lovett, P.S.
 J. Bacteriol. 158, 784-790, 1984
 A>Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
 A:Reference number: I39799; MUID:8412298; PMID:6327638
 A:Accession: I39799
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-30 <RES>
 A:Cross-references: UNIPROT:045356; GB:K01811; NID:g142647; PIDN:AAA22292.1; PID:g551696
 C:Superfamily: chloramphenicol acetyltransferase

Query Match 36.4%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENY 7
 ||||
 Db 6 DENY 9

RESULT 9
 B47607
 immunogenic protein MPB70/MPB80 - Mycobacterium bovis (strain BCG) (fragment)
 C:Species: Mycobacterium bovis
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: B47607
 R:Harboe, M.; Nagai, S.; Patarroyo, M.E.; Torres, M.L.; Ramirez, C.; Cruz, N.
 Infect. Immun. 52, 293-302, 1986
 A>Title: Properties of proteins MPB64, MPB70, and MPB80 of Mycobacterium bovis BCG.
 A:Reference number: A47607; MUID:86166829; PMID:3514457
 A:Accession: B47607
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-30 <HAR>

Query Match 36.4%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAA 10
 ||||
 Db 11 YAAA 14

RESULT 10
 F60529
 hemocyanin M1 - crayfish (Cherax destructor) (fragment)
 C:Species: Cherax destructor (yabby)
 C>Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 11-May-2000
 C:Accession: F60529
 R:Neuteboom, B.; Sierdsema, S.J.; Beintema, J.J.
 Comp. Biochem. Physiol. B 94, 587-592, 1989
 A>Title: The relationship between N-terminal sequences and immunological characterization
 A:Reference number: A60529; MUID:90151075; PMID:2620501
 A:Accession: F60529
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-32 <NEU>

Query Match 36.4%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDEN 6
 ||||
 Db 27 NDEN 30

RESULT 11
 PC1319
 large granule L9 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)

C:Species: Tachyplesus tridentatus
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1319
 R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iw.
 J. Biochem. 114, 307-316, 1993
 A>Title: Separation of large and small granules from horseshoe crab (Tachyplesus trident
 A:Reference number: PC1309; MUID:94110249; PMID:8282718
 A:Accession: PC1319
 A:Molecule type: protein
 A:Residues: 1-34 <SHI>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 36.4%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAV 11
 ||||
 Db 27 AAAV 30

RESULT 12
 A87279
 hypothetical protein CC0242 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87279
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B. J. Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
 n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87279
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-34 <STO>
 A:Cross-references: UNIPROT:Q9AB15; GB:AE005673; NID:g13421373; PIDN:AAK22229.1; GSPDB:
 C:Genetics:
 A:Gene: CC0242

Query Match 36.4%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAV 11
 ||||
 Db 24 AAAV 27

RESULT 13
 C94175
 hypothetical protein Vng0148h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C94175
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
 A>Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A94160; MUID:20504483; PMID:11016950
 A:Accession: C94175
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-36 <STO>
 A:Cross-references: UNIPROT:Q9HSN6; GB:AE004437; NID:g10579795; PIDN:AAG18767.1; GSPDB:
 C:Genetics:
 A:Gene: VNG0148H

Query Match 36.4%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|
|
|
|
DB 16 AAAY 19

RESULT 14

A32000
somatostatin, pancreatic - sea lamprey
C/Species: Petromyzon marinus (sea lamprey)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: A32000
R/Andrews, P.C.; Pollock, H.G.; Elliott, W.M.; Youson, J.H.; Plisetskaya, E.M.
J. Biol. Chem. 263, 15809-15814, 1988
A/Title: Isolation and characterization of a variant somatostatin-14 and two related somatostatin-14 fragments
A/Reference number: A32000; MUID:89008497; PMID:2902094
A/Accession: A32000
A/Molecule type: protein
A/Residues: 1-37 <AND>
A/Cross-references: UNIPROT:P21779
C/Superfamily: somatostatin
C/Keywords: neuropeptide

Query Match 36.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|
|
|
|
DB 4 AAAY 7

RESULT 15

S17684
thaumatin homolog 2 - barley
C/Species: Hordeum vulgare (barley)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S17684
R/Hejgaard, J.; Jacobsen, S.; Svendsen, I.
FEBS Lett. 291, 127-131, 1991
A/Title: Two antifungal thaumatin-like proteins from barley grain.
A/Reference number: S17573; MUID:92037994; PMID:1936240
A/Accession: S17684
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-37 <HEJ>
A/Cross-references: UNIPROT:P33045
C/Superfamily: thaumatin I

Query Match 36.4%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAAY 11
|
|
|
|
DB 15 AAAY 18

Search completed: May 5, 2005, 18:25:28
Job time : 23.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:00:34 ; Search time 101.333 Seconds
(without alignments)
41.984 Million cell updates/sec

Title: US-10-827-133-8
Perfect score: 11
Sequence: 1 AANDENYAAAV 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	11	2	ABB84403 E. coli d
2	8	72.7	11	6	AA016101 C-termina
3	8	72.7	11	7	AD848279 TAT depen
4	8	72.7	11	7	AD50155 S. enteri
5	8	72.7	12	5	AAE28994 Peptide u
6	6	54.5	6	7	ADJ33753 Bacteriolo
7	5	45.5	9	8	ADN63606 HLA bindi
8	5	45.5	14	7	ADD23307 Breast ca
9	5	45.5	21	8	ADK50911 Human C35
10	5	45.5	22	7	ADC33576 Fusion pe
11	5	45.5	30	2	AAK37123 Decarbamy
12	5	45.5	31	7	ADA07577 Human sec
13	5	45.5	31	8	ADN41386 Novel hum
14	5	45.5	32	4	AAE1562 Peptide W
15	5	45.5	32	4	AAE61569 Peptide W
16	5	45.5	32	4	AAE61568 Peptide W
17	5	45.5	32	4	AAE61559 Peptide W
18	5	45.5	33	8	ADK50912 Human C35
19	5	45.5	37	4	AAE61571 Peptide w
20	5	45.5	41	2	AAK33241 Human bet
21	5	45.5	41	3	AAE21594 Cone snai
22	4	36.4	4	2	AAE55338 Inhibitor
23	4	36.4	4	2	AAW52602 Serine pr
24	4	36.4	4	4	AAE97630 Elastase
25	4	36.4	5	2	AAE12715 Pentapept

26	4	36.4	5	2	AAE51579	Mimotope
27	4	36.4	5	2	AAE47436	Cyclic pe
28	4	36.4	5	2	AAE69947	Pentameri
29	4	36.4	5	2	AAE98693	Peptide 7
30	4	36.4	5	2	AAE99480	Encoded r
31	4	36.4	5	2	AAW51637	Peptide u
32	4	36.4	5	2	AAW50861	Cyclic pe
33	4	36.4	5	2	AAW87434	Peptide d
34	4	36.4	5	4	AAE62278	Linker se
35	4	36.4	5	7	ADP53386	Adeno-ass
36	4	36.4	5	7	ADP53411	Adeno-ass
37	4	36.4	6	2	AAE99967	ClaH12 T-
38	4	36.4	6	2	AAE15883	Peptide d
39	4	36.4	6	2	AAW83713	Peptide s
40	4	36.4	6	2	AAW87408	Peptide d
41	4	36.4	6	2	AAW87399	Peptide d
42	4	36.4	6	8	ADE97522	Immunogen
43	4	36.4	7	2	AAW87439	Peptide d
44	4	36.4	7	5	AAW49635	Human bet
45	4	36.4	7	5	AAW47146	S chrysom

ALIGNMENTS

RESULT 1
ABB84403
ID ABB84403 standard; peptide; 11 AA.
XX ABB84403;
XX
XX 21-OCT-2002 (first entry)
XX
XX E. coli derived aberrant protein C-terminal peptide motif.
XX
XX Tumour antigen; murine; vaccine; cellular immune response; immunogen;
XX cancer; tumour.
XX Escherichia coli.
XX
XX US6287569-B1.
XX
XX 11-SEP-2001.
XX
XX 06-APR-1998; 98US-00056105.
XX
XX 10-APR-1997; 97US-0043467P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Kipps TJ, Wu Y;
XX
XX WPI; 1998-583198/49.
XX
XX Generating cellular immune response in patient to target protein -
XX comprises introducing vector with nucleotide sequence encoding immunogen
XX comprising protein processing signal into cell of patient.
XX
XX Example 5; Col 6; 61pp; English.

This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents an E. coli aberrant protein motif described in the method of the invention. Note: The information in this spec has been previously disclosed in WO199845444 however this spec

[illegible]

PD 28-AUG-2003.
 XX
 XX 19-FEB-2003; 2003WO-BP001676.
 XX
 XX 19-FEB-2002; 2002US-0357103P.
 PR 05-JUL-2002; 2002US-0394777P.
 XX
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA
 XX
 XX Bumann D;
 PI
 XX WPI; 2003-712619/67.
 DR
 XX New bacterial promoters active in vivo, useful in preparation of live,
 PT recombinant vaccines, also mutated Shine-Dalgarno sequences for
 PT modulating promoter activity.
 XX
 XX Disclosure; SEQ ID NO 2; 92pp; German.
 PS
 XX This invention describes novel active promoters described as 4.5G, A.8H,
 CC 1f, 3g, 1c, 2a, 4a, 10g, 12b, A.2A, A.7A, A.9D, A.10F, A.11B, A.11H,
 CC A.12A, A.12G, CLII.4C, CLII.3A, CLII.9B, CLII.11C, CLII.12C, 3-2B, 3-4F,
 CC 3.6B, 3.9A, 3.9E, A.11A, A.8.B, CLII.5A, 4.4G or A.1A and their mutants.
 CC The invention also describes recombinant bacteria that contains the
 CC promoter, operatively linked to a heterologous nucleic acid, live vaccine
 CC containing the bacteria and constructs with mutations in the Shine
 CC Dalgarno sequence. The target bacteria are those used as carriers in live
 CC vaccines, particularly salmonella or probiotic bacteria. The new
 CC promoters are used in preparation of live vaccines, especially for
 CC expression of heterologous antigen. Also the mutated Shine-Dalgarno
 CC sequence is used to modify (especially reduce) the activity of regulatory
 CC gene elements, for targeted optimisation of the properties of recombinant
 CC live vaccines. The new promoters (and/or mutated Shine-Dalgarno
 CC sequences) provide targeted modulation of gene expression, including,
 CC where the promoter has high activity both in vivo and in vitro induction
 CC of a two-phase immune response.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 72.7%; Score 8; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.096; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AANDENYA 8
 Db |||||
 1 AANDENYA 8

RESULT 5
 AAE28994
 ID AAE28994 standard; peptide; 12 AA.
 XX
 XX AAE28994;
 AC
 XX 27-JAN-2003 (first entry)
 DT
 XX Peptide used in the exemplification of the invention.
 XX
 XX Vector; prokaryotic cell.
 XX
 XX Unidentified.
 OS
 XX WO200272847-A2.
 PN
 XX
 XX 19-SEP-2002.
 PD
 XX 22-FEB-2002; 2002WO-US005069.
 PF
 XX 09-MAR-2001; 2001US-0274384P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Paegle ES, Reilly D, Yansura DG;
 PI

XX WPI; 2002-723363/78.
 DR
 XX New vector comprising anti-termination nucleic acid or RNA encoding the
 PT polypeptide with a non-lambda promoter, useful for producing human
 PT thrombospondin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide.
 XX
 XX Example 2; Page 32; 70pp; English.
 PS
 XX The invention relates to vectors for producing a polypeptide heterologous
 CC to prokaryotic cells and method for producing the polypeptide. The method
 CC is useful for producing a polypeptide heterologous to prokaryotic cells.
 CC The present sequence is a peptide used in the exemplification of the
 CC invention
 XX
 XX Sequence 12 AA;
 SQ

Query Match 72.7%; Score 8; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AANDENYA 8
 Db |||||
 2 AANDENYA 9

RESULT 6
 ADL33753
 ID ADL33753 standard; protein; 6 AA.
 XX
 XX ADL33753;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Bacteriophage T7 ssrA peptide.
 DE
 XX protein solubility; coxsackievirus and adenovirus receptor; CAR;
 KW Bacteriophage T7; ssrA peptide.
 KW
 XX Enterobacteria phage T7.
 OS
 XX US2003134352-A1.
 PN
 XX 17-JUL-2003.
 PD
 XX 04-JAN-2002; 2002US-00037243.
 PF
 XX 04-JAN-2002; 2002US-00037243.
 PR
 XX (FREI/) FREIMUTH P I.
 PA (ZHAN/) ZHANG Y.
 PA (HOWI/) HOWITT J A.
 XX
 XX Freimuth PI, Zhang Y, Howitt JA;
 PI
 XX WPI; 2003-897262/82.
 DR
 XX Enhancing the solubility of, and promoting the adoption of native
 PT conformation in a recombinantly expressed polypeptide comprises
 PT expressing the polypeptide as a fusion protein with a charged N- or C-
 PT terminal extension.
 XX
 XX Disclosure; Page 9; 21pp; English.
 PS
 XX The invention relates to a method of enhancing the solubility of, and
 CC promoting the adoption of native protein conformation of a recombinantly
 CC expressed polypeptide by expressing the polypeptide as a fusion protein
 CC including a peptide extension with: net negative charge (not peptide T7A)
 CC positioned at the carboxy terminus; or net charge +2 to -20, positioned
 CC at the amino terminus. The nucleic acids encoding the polypeptide of
 CC interest and the extension are fused and inserted into an expression
 CC vector which is then introduced into a host cell in which the polypeptide
 CC is produced. The polypeptide is especially one that is substantially

CC insoluble or inactive when expressed recombinantly without the peptide
CC extension. The present sequence represents Bacteriophage T7 ssRNA peptide,
CC used in a fusion to demonstrate the method of the invention.

XX SQ Sequence 6 AA;
Query Match 54.5%; Score 6; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDEN 6
| | | | |
Db 1 AANDEN 6

RESULT 7
ADN63606
ID ADN63606 standard; peptide; 9 AA.
XX
XX ADN63606;
AC
XX 01-JUL-2004 (first entry)
DT
XX
XX HLA binding peptide #206.
DE
XX
XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
KW prostate specific antigen; prostate specific membrane antigen;
KW hepatitis B virus antigen; hepatitis C virus antigen;
KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
KW chondyroma acuminatum.
XX
XX Unidentified.
OS
XX WO2004031211-A2.
XX
XX 15-APR-2004.
PD
XX
XX 03-OCT-2003; 2003WO-US031308.
XX
XX 03-OCT-2002; 2002US-0416207P.
XX
XX 08-OCT-2002; 2002US-0417269P.
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX Sidney J, Southwood S, Sette A;
PI
XX WPI; 2004-347953/32.
DR
XX
XX New composition of peptides and nucleic acids capable of binding Major
PT Histocompatibility Complex molecules, useful for diagnosing, preventing
PT or treating viral infections or cancer, such as prostate cancer,
PT hepatitis B or AIDS.
XX
XX Claim 1; SEQ ID NO 206; 186pp; English.

CC The invention relates to a novel composition comprising one or more
CC peptides or nucleic acids encoding an HLA binding peptide. The
CC composition further comprises an HTL epitope. It also comprises a spacer
CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
CC are incorporated as part of a liposome. The peptide is from an antigen
CC selected from prostate specific antigen (PSA), prostate specific membrane
CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
CC Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT); p53,
CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
CC (TKP). The composition is useful for preventing or treating viral
CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyroma
CC acuminatum. The composition is also be used for diagnosing such diseases.
CC This sequence represents a peptide of the invention.

XX SQ Sequence 9 AA;
Query Match 45.5%; Score 5; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAAAV 11
| | | | |
Db 5 YAAAV 9

RESULT 8
ADD23307
ID ADD23307 standard; peptide; 14 AA.
XX
XX ADD23307;
AC
XX 15-JAN-2004 (first entry)
DT
XX
XX Breast cancer membrane protein (BCMP) peptide SEQ ID NO:556.
DE
XX
XX breast cancer; screening; diagnosis; breast cancer therapy;
KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
KW
XX Homo sapiens.
OS
XX WO2003087831-A2.
XX
XX 23-OCT-2003.
PD
XX
XX 10-APR-2003; 2003WO-GB001559.
XX
XX 11-APR-2002; 2002GB-00008331.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Hudson LJ, Stamps AC, Terrett JA;
XX WPI; 2003-845381/78.
DR
XX
XX Screening, diagnosing and/or treating breast cancer by detecting a change
PT in expression or activity of a breast cancer membrane protein (BCMP)
PT polypeptide or encoding nucleic acid molecule.
XX
XX Example; SEQ ID NO 556; 81pp; English.

CC The present invention describes a method of screening for and/or
CC diagnosing breast cancer in a subject, and/or monitoring the
CC effectiveness of breast cancer therapy. The method comprises detecting
CC and/or quantifying in a biological sample obtained from the subject a
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
CC molecule. Also described: (1) an antibody, its functionally-active
CC fragment, derivative or analogue, that specifically binds to one or more
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
CC reagent specific for an BCMP polypeptide, reagents and instructions for
CC use; (3) a method for screening for anti-breast cancer agents that
CC interact with the BCMP polypeptide, comprising contacting the polypeptide
CC with a candidate agent, and determining whether or not the candidate
CC agent interacts with the polypeptide; (4) a method for screening for anti
CC breast cancer agents that modulate the expression or activity of an BCMP
CC polypeptide or the nucleic acid molecule cited above, comprising
CC comparing the expression or activity of the polypeptide or nucleic acid
CC molecule, in the presence and absence of a candidate agent or in the
CC presence of a control agent, and determining whether the candidate agent
CC causes the expression or activity of the polypeptide or nucleic acid
CC molecule to change; and (5) an agent identified by the method of (3) or
CC (4), which interacts with the polypeptide or causes the expression or
CC activity of the polypeptide, or the expression of the nucleic acid
CC molecule to change. BCMPs have cytostatic activities, and can be used in
CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
CC their derivatives, are useful in the manufacture of a medicament for the
CC treatment of breast cancer, where the composition is a vaccine. The

CC present sequence represents a BCMP peptide which is used in the
 CC exemplification of the present invention.

SQ Sequence 14 AA;

Query Match 45.5%; Score 5; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAAV 11
 |||||
 Db 7 YAAAV 11

RESULT 9

ADK50911
 ID: ADK50911 standard; peptide; 21 AA.

AC ADK50911;

XX 04-NOV-2004 (first entry)

DT Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 123.

DE C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma;
 KW human; Kaposi FGF signal sequence h region MST; cell-penetrating;
 KW fibroblast growth factor; membrane-translocating signal.

XX Homo sapiens.
 OS Unidentified.

XX WO2003104428-A2.

PN 18-DEC-2003.

XX 10-JUN-2003; 2003WO-US018252.

XX 10-JUN-2002; 2002US-0386738P.

PR 11-DEC-2002; 2002US-0432241P.

XX 23-APR-2003; 2003US-0464650P.

XX (VACC-) VACCINEX INC.

PA (UYRP) UNIV. ROCHESTER.

XX Zauderer M, Evans EE, Borrello MA;

XX WPI; 2004-062349/06.

XX Novel C35 polypeptide useful for formulation of immunogenic composition
 PT to induce antibodies and cell-mediated immunity against tumor cells.

XX Disclosure; Page 223; 626pp; English.

CC The invention relates to a novel isolated polypeptide comprising or
 CC consisting of two or more C35 peptide epitopes. The polypeptide of the
 CC invention demonstrates cytostatic activity and may be useful for the
 CC formulation of an immunogenic composition, such as a vaccine, to induce
 CC antibodies and cell-mediated immunity against target cells such as tumour
 CC cells. Furthermore, the polypeptide and its analogues may be useful as
 CC prognostic markers for carcinoma, such as human breast or bladder
 CC carcinoma. The current sequence is that of human C35 / Kaposi FGF
 CC (fibroblast growth factor) signal sequence MST (membrane-translocating
 CC sequence) cell-penetrating polypeptide of the invention.

SQ Sequence 21 AA;

Query Match 45.5%; Score 5; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAAAV 11
 |||||
 Db 8 YAAAV 12

RESULT 10

ADC33576

XX ADC33576 standard; peptide; 22 AA.

AC ADC33576;

XX 18-DEC-2003 (first entry)

DT Fusion peptide fragment #SEQ ID 50.

DE Fused polypeptide; autoantigen; tolerogen; neurodegenerative disease.

XX synthetic.

XX JP2003000284-A.

XX 07-JAN-2003.

XX 11-APR-2002; 2002JP-00108834.

XX 16-APR-2001; 2001US-00836433.

XX (NICH-) JAPAN CHEM RES CO LTD.

XX WPI; 2003-461481/44.

XX A hybrid protein for autoimmune diseases, a polynucleotide, an expression
 PT vector, a fused polypeptide, a drug composition, a host cell, preparation
 PT of an autoantigen fused polypeptide.

XX Example 6; SEQ ID NO 50; 30pp; Japanese.

XX The invention relates to a polynucleotide encoding a fused polypeptide
 CC comprising a polynucleotide encoding at least one autoantigen peptide
 CC fused inframe to a polynucleotide encoding a tolerogen polynucleotide. Also
 CC disclosed is an expression vector containing the above polynucleotide
 CC linked operably to at least one transcription-controlling element, a
 CC fused polypeptide expressed from the above expression vector, and a drug
 CC composition containing the above fused polypeptide and a
 CC pharmacologically allowable carrier. The autoantigen fused polypeptide
 CC can be used for treating neurodegenerative diseases. Sequences given in
 CC records ADC3527-{seqid:53} represent fusion peptides of the invention,
 CC their fragments, DNA encoding them and primers.

XX Sequence 22 AA;

Query Match 45.5%; Score 5; DB 7; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ANDEN 6

Db 11 ANDEN 15

RESULT 11

AAR37123

ID AAR37123 standard; peptide; 30 AA.

AC AAR37123;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 17-NOV-1994 (first entry)

XX Decarbamylase N-terminal fragment.

XX N-terminal; decarbamylase; enzyme; Comamonas; sp. E222C; Blastobacter;
 KW sp. Al7p-4; Rhizobium; sp. KKK1415; D-alpha-amino acid;
 KW N-carbamyl-D-alpha-amino acid; neutral; alkaline; semi-synthetic;
 KW penicillin; cephalosporin.

```

XX OS Comamonas sp; E222C.
XX FH Key Location/Qualifiers
XX FT Misc-difference 20 /note= "Uncertainty regarding this position"
XX FT Misc-difference 26 /note= "Uncertainty regarding this position"
XX XX
XX PN W09408030-A1.
XX XX
XX PD 14-APR-1994.
XX XX
XX PF 01-OCT-1993; 93WO-JP001408.
XX XX
XX PR 05-OCT-1992; 92JP-00265914.
XX XX
XX PA (KANF ) KANEGAFUCHI CHEM IND CO LTD.
XX PI Yamada H, Shimizu S, Ikenaka Y, Yajima K, Yamada Y, Nanba H;
XX PI Takano M, Takahashi S;
XX XX
XX DR WPI; 1994-135591/16.
XX XX
XX PT D-alpha-aminoacid prodn using decarboxylase enzyme - can be efficiently
XX PT conducted under neutral to alkaline conditions, giving prod useful in
XX PT prodn of semi-synthetic penicillin and cephalosporin cpds.
XX XX
XX PS Claim 14; Page 33; 52pp; Japanese.
XX XX
XX CC The sequences given in AAR37123-25 represent the N-terminal fragments of
XX CC the decarboxylase enzyme of the invention derived from Comamonas sp.
XX CC E222C, Blastobacter sp. A17p-4 and Rhizobium sp. KNK1415 respectively.
XX CC These enzymes may be used in the production of D-alpha-amino acids by
XX CC treating N-carbamyl-D-alpha-amino acids with the enzyme which is produced
XX CC by a microorganism in an aqueous medium. The decarboxylase is efficient
XX CC under neutral to alkaline conditions and may be used in the production of
XX CC semi-synthetic penicillin and cephalosporin. (Updated on 25-MAR-2003 to
XX CC correct FN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 30 AA;

Query Match 45.5%; Score 5; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 5 NYAAA 9

RESULT 12
ADA07577
ID ADA07577 standard; peptide; 31 AA.
XX AC
XX AC ADA07577;
XX DT
XX DT 06-NOV-2003 (first entry)
XX DE
XX DE Human secreted protein from gene 35, peptide #6.
XX KW Immunosuppressive; dermatological; antiinflammatory; antiallergic;
XX KW antiarthritic; human; autoimmune disease; autoimmune disorder; lupus;
XX KW transplant rejection; allergic reaction; arthritis;
XX KW squamous cell E48 antigen.
XX OS Homo sapiens.
XX XX
XX PN US2003064412-A1.
XX PD
XX PD 03-APR-2003.
XX PF
XX PF 30-OCT-2001; 2001US-00984490.

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XX 08-JUL-1997; 97US-0051916P.
XX PR 08-JUL-1997; 97US-0051918P.
XX PR 08-JUL-1997; 97US-0051919P.
XX PR 08-JUL-1997; 97US-0051920P.
XX PR 08-JUL-1997; 97US-0051925P.
XX PR 08-JUL-1997; 97US-0051926P.
XX PR 08-JUL-1997; 97US-0051928P.
XX PR 08-JUL-1997; 97US-0051929P.
XX PR 08-JUL-1997; 97US-0051930P.
XX PR 08-JUL-1997; 97US-0051931P.
XX PR 08-JUL-1997; 97US-0051932P.
XX PR 08-JUL-1997; 97US-0052732P.
XX PR 08-JUL-1997; 97US-0052733P.
XX PR 08-JUL-1997; 97US-0052793P.
XX PR 08-JUL-1997; 97US-0052795P.
XX PR 08-JUL-1997; 97US-0052803P.
XX PR 18-AUG-1997; 97US-0055684P.
XX PR 18-AUG-1997; 97US-0055722P.
XX PR 18-AUG-1997; 97US-0055723P.
XX PR 18-AUG-1997; 97US-0055947P.
XX PR 18-AUG-1997; 97US-0055948P.
XX PR 18-AUG-1997; 97US-0055949P.
XX PR 18-AUG-1997; 97US-0055950P.
XX PR 18-AUG-1997; 97US-0055953P.
XX PR 18-AUG-1997; 97US-0055954P.
XX PR 18-AUG-1997; 97US-0055964P.
XX PR 18-AUG-1997; 97US-0055984P.
XX PR 18-AUG-1997; 97US-0056360P.
XX PR 12-SEP-1997; 97US-0058660P.
XX PR 12-SEP-1997; 97US-0058661P.
XX PR 12-SEP-1997; 97US-0058664P.
XX PR 12-SEP-1997; 97US-0058785P.
XX PR 07-JUL-1998; 98WO-US013684.
XX PR 08-JAN-1999; 99US-00227357.
XX (FISC/) FISCHER C L.
XX (ROSE/) ROSEN C A.
XX (SOPP/) SOPPET D R.
XX (RUBE/) RUBEN S M.
XX (KIYA/) KYAW H.
XX (LIYI/) LI Y.
XX (ZENG/) ZENG Z.
XX (LAFLE/) LAFLEUR D W.
XX (MOOR/) MOORE P A.
XX (SHIY/) SHI Y.
XX (OLSE/) OLSEN H S.
XX (EBNE/) EBNER R.
XX (BREW/) BREWER L A.
XX Fischer CL, Rosen CA, Soppet DR, Ruben SM, Kyaw H, Li Y, Zeng Z;
XX Lafleur DW, Moore PA, Shi Y, Olsen HS, Ebner R, Brewer LA;
XX WPI; 2003-540785/51.
XX Novel antibody which specifically binds to a secreted protein useful for
XX diagnosing and treating lupus, arthritis, allergic reactions, arthritis.
XX Disclosure; Page 26; 355pp; English.
XX The invention relates to an isolated antibody or its portion that
XX specifically binds to a protein that shares sequence homology with human
XX squamous cell E48 antigen, and consists of amino acid residues 21-116 or
XX 1-116 the protein appearing as ADA07417 (one of 123 disclosed novel human
XX secreted proteins encoded by 123 novel genes), or a protein consisting of
XX amino acid sequence of secreted or full-length polypeptide encoded by
XX HLHFP03 cDNA contained in ATCC Deposit No. 209126. The antibody is
XX produced by immunising an animal with amino acid residues 21-116 of
XX ADA07417, or with a protein consisting of amino acid sequence of the
XX secreted polypeptide encoded by the HLHFP03 cDNA contained in ATCC
XX Deposit No. 209126, respectively. Also included are an isolated cell that
XX produces the antibody and a hybridoma that produces the antibody. The
XX antibody is a monoclonal, polyclonal, chimeric, humanised or human

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CC antibody. Optionally, the antibody is a Fab fragment, and is labelled by
 CC a label chosen from enzyme label, a radioisotope, and a fluorescent
 CC label. The antibody is useful as a probe for differential identification
 CC of tissues or cell types in which ADA07417 is expressed. The antibody is
 CC also for diagnosis and treatment of autoimmune diseases and disorders,
 CC such as lupus, transplant rejection, allergic reactions, and arthritis.
 CC The present sequence is a peptide/protein derived from one of the 123
 CC novel secreted proteins.

XX Sequence 31 AA;

Query Match 45.5%; Score 5; DB 7; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10

DB 14 NYAAA 18

RESULT 13

ADN41386

ID ADN41386 standard; peptide; 31 AA.

XX AC ADN41386;

XX DT 17-JUN-2004 (first entry)

XX DE Novel human secreted protein fragment seqid 508.

XX KW immunomodulator; immunosuppressive; antiinflammatory; dermatological;
 KW antiarthritic; antirheumatic; neuroprotective; antianaemic; muscular;
 KW antiallergic; antiasthmatic; gastrointestinal; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; cardiant; cytostatic; nephrotropic;
 KW cardiovascular; respiratory; gene therapy; secreted protein;
 KW chromosome identification; hybrid mapping; gene expression control;
 KW immune system disorder; immunodeficiency; Chediak-Higashi syndrome;
 KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KW multiple sclerosis; haemolytic anaemia; myasthenia gravis;
 KW allergic reaction; asthma; inflammatory condition;
 KW inflammatory bowel disease; B cell stimulator; T cell activator;
 KW blood-related disorder; eosinophilia; thrombosis; thromboembolism;
 KW atherosclerosis; myocardial infarction; cancer; renal disorder;
 KW hyperproliferative disorder; cancer; renal disorder;
 KW chronic kidney failure; renal tubular acidosis; kidney stone;
 KW cardiovascular disorder; respiratory disorder; human.

XX OS Homo sapiens;

XX PN US2004044191-A1.

XX PD 04-MAR-2004.

XX PF 10-OCT-2001; 2001US-00973278.

XX PR 08-JUL-1997; 97US-0051916P.

PR 08-JUL-1997; 97US-0051918P.

PR 08-JUL-1997; 97US-0051919P.

PR 08-JUL-1997; 97US-0051920P.

PR 08-JUL-1997; 97US-0051923P.

PR 08-JUL-1997; 97US-0051926P.

PR 08-JUL-1997; 97US-0051928P.

PR 08-JUL-1997; 97US-0051929P.

PR 08-JUL-1997; 97US-0051930P.

PR 08-JUL-1997; 97US-0051933P.

PR 08-JUL-1997; 97US-0051932P.

PR 08-JUL-1997; 97US-0052732P.

PR 08-JUL-1997; 97US-0052733P.

PR 08-JUL-1997; 97US-0052793P.

PR 08-JUL-1997; 97US-0052795P.

PR 08-JUL-1997; 97US-0052803P.

PR 18-AUG-1997; 97US-0055684P.

PR 18-AUG-1997; 97US-0055722P.

PR 18-AUG-1997; 97US-0055723P.
 PR 18-AUG-1997; 97US-0055947P.
 PR 18-AUG-1997; 97US-0055948P.
 PR 18-AUG-1997; 97US-0055949P.
 PR 18-AUG-1997; 97US-0055950P.
 PR 18-AUG-1997; 97US-0055953P.
 PR 18-AUG-1997; 97US-0055954P.
 PR 18-AUG-1997; 97US-0055964P.
 PR 18-AUG-1997; 97US-0055984P.
 PR 18-AUG-1997; 97US-0056360P.
 PR 12-SEP-1997; 97US-0058660P.
 PR 12-SEP-1997; 97US-0058661P.
 PR 12-SEP-1997; 97US-0058664P.
 PR 12-SEP-1997; 97US-0058785P.
 PR 07-JUL-1998; 98WO-US013684.
 PR 08-JAN-1999; 99US-00227357.
 PR 13-OCT-2000; 2000US-0239899P.

XX (FISC/) FISCHER C L.

PA (ROSE/) ROSEN C A.

PA (SOPP/) SOPPET D R.

PA (RUBE/) RUBEN S M.

PA (KYAW/) KYAW H.

PA (LIY/) LI Y.

PA (ZENG/) ZENG Z.

PA (LAFL/) LAPLEUR D W.

PA (MOOR/) MOORE P A.

PA (SHIY/) SHI Y.

PA (OLSE/) OLSEN H.

PA (EBNE/) EBNER R.

PA (BIRS/) BIRSE C E.

XX

Fischer CL, Rosen CA, Soppet DR, Ruben SM, Kyaw H, Li Y, Zeng Z;
 Lafleur DW, Moore PA, Shi Y, Olsen H, Ebner R, Birse CE;

WPI; 2004-225733/21.

New isolated nucleic acid encoding human proteins, useful for treating,
 preventing or diagnosing e.g. rheumatoid arthritis, multiple sclerosis,
 anemia, inflammatory bowel disease, atherosclerosis, cancers, chronic
 kidney failure.

Disclosure; SEQ ID NO 508; 372pp; English.

The invention describes novel human secreted proteins and the nucleotides
 encoding them. The polynucleotides are useful in chromosome
 identification, for radiation hybrid mapping, in controlling gene
 expression, in gene therapy or as molecular weight markers. The
 polynucleotides and polypeptides are useful for diagnosing, treating or
 preventing diseases of the immune system, immunodeficiencies, e.g.
 Chediak-Higashi syndrome, autoimmune diseases, e.g. systemic lupus
 erythematosus, rheumatoid arthritis, multiple sclerosis, haemolytic
 anaemia or myasthenia gravis, allergic reactions, e.g. asthma,
 inflammatory conditions, e.g. inflammatory bowel disease. They can also
 be used as a stimulator of B cell responsiveness to pathogens or as an
 activator of T cells. The polynucleotides and polypeptides are also
 useful for treating or preventing blood-related disorders, e.g.
 eosinophilia, thrombosis, thromboembolism, atherosclerosis, myocardial
 infarction, unstable angina or anaemia. They can also be used for
 treating, preventing or diagnosing hyperproliferative disorders
 (cancers), renal disorders (chronic kidney failure, renal tubular
 acidosis or kidney stones), cardiovascular disorders or respiratory
 disorders. This is the amino acid sequence of a novel human secreted
 protein fragment. Note: This sequence is available in electronic format
 from the US patent office at
 ftp.segdata.uspto.gov/sequence.html?DocID=20040044191.

Sequence 31 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Length 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10
 PNI
 DB 14 NYAAA 18

RESULT 14

AAB61562
 ID AAB61562 standard; peptide; 32 AA.

XX AC AAB61562;

XX DT 03-APR-2001 (first entry)

XX DE Peptide WINZIPB4 used to identify hetero-associating peptides.

XX KW Hetero-associating coiled-coil peptide; heterodimerisation.

XX OS Unidentified.

XX PN WO200100814-A2.

XX PD 04-JAN-2001.

XX PF 26-JUN-2000; 2000WO-EP005922.

XX PR 25-JUN-1999; 99US-00344096.

XX PA (UYZU-) UNIV ZUERICH.

XX PI Plueckthun A, Arndt K, Mueller K, Pelletier J;

XX DR WPI; 2001-137954/14.

XX PT Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.

XX PS Claim 6; Page 40; 56pp; English.

XX CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention

XX SQ Sequence 32 AA;

Query Match 45.5%; Score 5; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENYA 8
 PNI
 DB 13 DENYA 17

RESULT 15

AAB61569
 ID AAB61569 standard; peptide; 32 AA.

XX AC AAB61569;

XX DT 03-APR-2001 (first entry)

XX DE Peptide WINZIPB11 used to identify hetero-associating peptides.

XX KW Hetero-associating coiled-coil peptide; heterodimerisation.

XX OS Unidentified.

XX WO200100814-A2.
 PN
 XX
 PD 04-JAN-2001.

XX 26-JUN-2000; 2000WO-EP005922.

XX PR 25-JUN-1999; 99US-00344096.

XX PA (UYZU-) UNIV ZUERICH.

XX PI Plueckthun A, Arndt K, Mueller K, Pelletier J;

XX DR WPI; 2001-137954/14.

XX PT Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.

XX PS Claim 6; Page 41; 56pp; English.

XX CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention

XX SQ Sequence 32 AA;

Query Match 45.5%; Score 5; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENYA 8
 PNI
 DB 13 DENYA 17

Search completed: May 5, 2005, 18:18:04
 Job time : 104.333 secs